

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:40:11 ; Search time 12 Seconds
(without alignments)
1050.081 Million cell updates/sec

Title: US-10-068-564-5

Perfect score: 1239
Sequence: 1 MSNPRSLSEEEKYDMSGALAA.....KARKNPEIQSLTKRRLYLQ 242

Scoring table: ELOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	99.6	242	1	ICEE_HUMAN P31944 homo sapien
2	934.5	75.4	257	1	ICEE_MOUSE O89004 mus musculu
3	305	24.6	424	1	ICEE_CHICK Q98943 gallus gall
4	295	23.8	435	1	ICEE_MOUSE P29594 mus musculu
5	289	23.3	435	1	ICEE_HUMAN P42575 homo sapien
6	279.5	22.6	277	1	ICEE_RAT P55213 rattus norv
7	277.5	22.4	277	1	ICEE_CRILLO P60431 cricetus
8	273.5	22.1	277	1	ICEE_MOUSE P70677 mus musculu
9	272.5	22.0	277	1	ICEE_HUMAN P42574 homo sapien
10	270	21.8	303	1	ICEE_MOUSE P97864 mus musculu
11	260	21.0	303	1	ICEE_MOUSE P55210 homo sapien
12	256	20.7	303	1	ICEE_HUMAN P42573 caenorhabdi
13	248.5	20.1	503	1	ICED3_MOUSE P55214 mesocricetu
14	247.5	20.0	339	1	ICED3_MOUSE P55210 homo sapien
15	246.5	19.9	479	1	ICED3_MOUSE P55210 homo sapien
16	245	19.8	479	1	ICED3_MOUSE P55210 homo sapien
17	240.5	19.4	276	1	ICED3_MOUSE P55210 homo sapien
18	239.5	19.3	299	1	ICED3_MOUSE P55210 homo sapien
19	237.5	19.2	299	1	ICED3_MOUSE P55210 homo sapien
20	236.5	19.1	404	1	ICED3_MOUSE P55210 homo sapien
21	233	18.8	480	1	ICED3_MOUSE P55210 homo sapien
22	227	18.3	282	1	ICED3_MOUSE P55210 homo sapien
23	226.5	18.3	382	1	ICED3_MOUSE P55210 homo sapien
24	226	18.2	404	1	ICED3_MOUSE P55210 homo sapien
25	225.5	18.2	323	1	ICED3_MOUSE P55210 homo sapien
26	225	18.2	323	1	ICED3_MOUSE P55210 homo sapien
27	222.5	18.0	386	1	ICED3_MOUSE P55210 homo sapien
28	222	17.9	521	1	ICED3_MOUSE P55210 homo sapien
29	221.5	17.9	521	1	ICED3_MOUSE P55210 homo sapien
30	218.5	17.6	402	1	ICED3_MOUSE P55210 homo sapien
31	218	17.6	373	1	ICED3_MOUSE P55210 homo sapien
32	217.5	17.6	402	1	ICED3_MOUSE P55210 homo sapien
33	213.5	17.2	312	1	ICED3_MOUSE P55210 homo sapien

34	212.5	17.2	405	1	IIIC_HORSE Q9TV13 equus cabal
35	211	17.0	410	1	IIIC_FELCA Q9MZV6 felis silve
36	209	16.9	404	1	IIIC_PIG Q9NZ11 sus scrofa
37	205.5	16.6	377	1	ICED4_HUMAN P49667 homo sapien
38	196	15.8	377	1	ICED4_BOVIN O75601 bos taurus
39	193.5	15.6	419	1	ICED_MOUSE O08736 mus musculu
40	104.5	8.4	484	1	CEIA_MOUSE O35732 m casp8 and
41	97	7.8	1051	1	APSB_EMBNI O60039 emericella
42	96	7.7	527	1	APSB_PSESM O87671 pseudomonas
43	95.5	7.7	862	1	CSP2_MACPA Q9NE52 macaca fasc
44	95.5	7.7	2104	1	MYS3_SCHPO O14157 schizosach
45	94	7.6	480	1	CFLA_HUMAN O15519 h casp8 and

ALIGNMENTS

RESULT 1
ICED_HUMAN STANDARD; PRT; 242 AA.
ID ICED_HUMAN
AC P31944; 095823; (Rel. 26, Created)
DT 01-JUL-1993
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
GN CASP14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=22168928; PubMed=12181750;
RA Pistrutto G., Jost M., Srinivasula S.M., Baffa R., Poyet J.-L.,
RA Kari C., Lazebnik Y., Rodeck U., Alnemri E.S.;
RT "Expression and transcriptional regulation of caspase-14 in simple
RT and complex epithelia".
RL Cell Death Differ. 9:995-1006(2002).
[2]
RN SEQUENCE OF 68-74; 137-147 AND 154-162.
RP TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1266667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.; 145 proteins recorded in the two-dimensional gel
RT "Microsequences of normal human epidermal keratinocytes".
RL Electrophoresis 13:960-969(1992).
CC -!- FUNCTION: May be involved in the death receptor and granzyme B
CC apoptotic pathways. May function as a downstream signal transducer
CC of cell death.
CC -!- SUBUNIT: May dimerize with large prodomain caspases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC
CC EMBL; AF097874; AAD16173.1; -
CC PIR; J07517; J07517.
CC HSSP; P29466; 1ICE.
DR Aarhus/Ghent-2DPAGE; 6109; IEF.
DR MEROPS; C14.018; -
DR Genew; HGNC:1502; CASP14.
DR MIM; 605848; -
DR GO; GO:0004199; F:caspase activity; TAS.
DR GO; GO:0008544; P:epidermal differentiation; TAS.
DR InterPro; IPR002138; ICE_p10.

DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
 DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR Hydrolase; Thiol protease; Apoptosis; Zymogen.
 FT CHAIN 1 146
 FT CHAIN 147 242
 FT ACT_SITE 89 89
 FT ACT_SITE 132 132
 SQ SEQUENCE 242 AA; 27679 MW; E539FB78DD08A2 CRC64;

Query Match 99.6%; Score 1234; DB 1; Length 242;
 Best Local Similarity 99.6%; Pred. No. 5.8e-92;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDLLEHMFROAPESTMRKDPPTAQ 60
 Db 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDLLEHMFROAPESTMRKDPPTAQ 60
 QY 61 FOEIELEKFOQALIDREDEPVSCAFVLMAGREGFLKGEDEGMVLEMLFEALNNKNCAL 120
 Db 61 FOEIELEKFOQALIDREDEPVSCAFVLMAGREGFLKGEDEGMVLEMLFEALNNKNCAL 120
 QY 121 RAKPKVYIIACRGEGDPEFTVGGDEIVWIKDSPTITTYDHALHVSIVGEGYAYRH 180
 Db 121 RAKPKVYIIACRGEGDPEFTVGGDEIVWIKDSPTITTYDHALHVSIVGEGYAYRH 180
 QY 181 DQKGSCEIQTLDVFTFKRKHIIELTEVTRMAEALVOEGARKNPEIOSTLRRLY 240
 Db 181 DQKGSCEIQTLDVFTFKRKHIIELTEVTRMAEALVOEGARKNPEIOSTLRRLY 240
 QY 241 LQ 242
 Db 241 LQ 242

RESULT 2
 ICEE MOUSE STANDARD; PRT; 257 AA.
 AC 089094;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (Mini-ICE) (MICE).
 GN CASP14.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=99040667; PubMed=9823333;
 RA Ahmad M., Srinivasula S.M., Hegde R., Mukattash R.,
 RA Fernandes-Alnemri T., Alnemri E.S.,
 RT "Identification and characterization of murine caspase-14, a new
 member of the caspase family.";
 RL Cancer Res. 58:5201-5205(1998).
 RN [2] Nov 1998
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Embryo;
 RX MEDLINE=99222069; PubMed=10203698;
 RA Van de Craen M., Van Loo G., Pype S., Van Criekinge W.,
 RA Van den Brande I., Molemans F., Fiers W., Declercq W.,
 RT "Identification of a new caspase homologue: caspase-14.";
 RL Cell Death Differ. 5:838-846(1998).

RM [3]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.
 RX MEDLINE=99009076; PubMed=9792675;
 RA Hu S., Snipas S.J., Vincenz C., Salvesen G., Dixit V.M.,
 RT "Caspase-14 is a novel developmentally regulated protease.";
 RL J. Biol. Chem. 273:29648-29653(1998).
 CC -1- FUNCTION: Seems to be involved in the death receptor and granzyme
 B apoptotic pathways. May function as a downstream signal
 transducer of cell death. May play a role in ontogenesis and skin
 physiology.
 CC -1- SUBUNIT: May dimerize with large prodomain caspases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain
 and kidney.
 CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE
 TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 PROTEASE.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
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DR EMBL; AF092997; AAC63364.1; -;
 DR EMBL; AJ007750; CA07678.1; -;
 DR HSSP; P29466; 1ICE.
 DR MEROPS; C14.018; -;
 DR MED; MG1.1335092; Casp14.
 DR GO; GO:0006917; P:induction of apoptosis; IDA.
 DR InterPro; IPR002138; ICE P10.
 DR InterPro; IPR001309; ICE p20.
 DR InterPro; IPR002398; Peptidase C14.
 DR Pfam; PF00656; Peptidase C14; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00115; CASc; 1.
 DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
 DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR Hydrolase; Thiol protease; Apoptosis; Zymogen.
 FT CHAIN 1 7
 FT CHAIN 8 257
 FT ACT_SITE 93 93
 FT ACT_SITE 136 136
 FT MUTAGEN C->A: DECREASE IN DEATH-INDUCING
 ACTIVITY.
 SQ SEQUENCE 257 AA; 29458 MW; A228D88DFA0B84 CRC64;

Query Match 75.4%; Score 934.5; DB 1; Length 257;
 Best Local Similarity 70.9%; Pred. No. 6.5e-68;
 Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDLLEHMFROAPESTMRKDPPTAQ 60
 Db 5 MSNPRSLSEEEKYDMSGALALILCVTKAREGSEEDLDLLEHMFROAPESTMRKDPPTAQ 60
 QY 61 FOEIELEKFOQALIDREDEPVSCAFVLMAGREGFLKGEDEGMVLEMLFEALNNKNCAL 120
 Db 65 FOEIELEKFOQALIDREDEPVSCAFVLMAGREGFLKGEDEGMVLEMLFEALNNKNCAL 124
 QY 121 RAKPKVYIIACRGEGDPEFTVGGDEIVWIKDSPTITTYDHALHVSIVGEGYAYRH 168
 Db 125 RAKPKVYIIACRGEGDPEFTVGGDEIVWIKDSPTITTYDHALHVSIVGEGYAYRH 183
 QY 169 YSTVEGYIAYHNDKSGSCFIQTLDVFTFKRKHIIELTEVTRMAEALVOEGARKNKTN 228
 Db 184 YSTVEGYIAYHNDKSGSCFIQTLDVFTFKRKHIIELTEVTRMAEALVOEGARKNKTN 243

Yr	229	PELOSTLRKRLVIO	242
Db	244	PEVOSTLRKRLVIO	257
RESULT 3			
ID	ICE2_CHICK	STANDARD;	PRT; 424 AA.
AC	Q98943;		
DT	01-NOV-1997	(Rel. 35, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DE	10-OCT-2003	(Rel. 42, Last annotation update)	
DE	Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).		
GN	CASP2 OR ICH1.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
CC	Gallus.		
CC	NCBI_TaxID=9031;		
CC	NCBI_TaxID=9031;		
CC	SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).		
CC	STRAIN=White leghorn; TISSUE=Ovarian granulosa;		
CC	MEDLINE=97368127; Pubmed=9224894;		
CC	Johnson A.L., Birdgham J.T., Bergeron L., Yuan J.;		
CC	"Characterization of the avian Ich-1 cDNA and expression of Ich-1L		
CC	mRNA in the hen ovary".		
CC	Gene 192:227-233(1997).		
CC	-I- FUNCTION: Involved in the activation cascade of caspases		
CC	responsible for apoptosis execution. Might function by either		
CC	activating some proteins required for cell death or inactivating		
CC	proteins necessary for cell survival (By similarity).		
CC	-I- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2;		
CC	Name=ICH-1L;		
CC	Isoid=Q98943-1; Sequence=Displayed;		
CC	Note=Only form found in the ovary;		
CC	Name=ICH-1S;		
CC	Isoid=Q98943-2; Sequence=VSP 000803, VSP 000804;		
CC	-I- PTM: Heterodimer of a small and a large subunit (By similarity).		
CC	-I- SIMILARITY: Belongs to peptidase family C14.		
CC	-I- SIMILARITY: Contains 1 CARD domain.		
CC	-----		
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CC	-----		
DR	EMBL; U64963; AAC29881.1; ALT_INIT.		
DR	HSSP; P42574; ICP3.		
DR	MEROBS; C14.006; -.		
DR	InterPro; IPR001315; CARD.		
DR	InterPro; IPR002108; ICE_P10.		
DR	InterPro; IPR001309; ICE_P20.		
DR	InterPro; IPR002398; Peptidase_C14.		
DR	Pfam; PF00619; CARD; 1.		
DR	Pfam; PF00656; Peptidase_C14; 1.		
DR	PRINTS; PR00376; IL1BCENZME.		
DR	SMART; SM00114; CARD; 1.		
DR	SMART; SM00115; CASC; 1.		
DR	PROSITE; PS50209; CARD; 1.		
DR	PROSITE; PS01122; CASPASE_CYS; 1.		
DR	PROSITE; PS01121; CASPASE_HIS; 1.		
DR	PROSITE; PS50207; CASPASE_P10; 1.		
DR	PROSITE; PS50208; CASPASE_P20; 1.		
KW	Hydrolase, Thiol protease, Apoptosis; Zymogen, Alternative splicing.		
FT	PROPEP 1	308	
FT	CHAIN 141	140	
FT	CHAIN 309	424	
FT	CASPASE-2 SUBUNIT P18 (BY SIMILARITY).		
FT	CASPASE-2 SUBUNIT P13 (BY SIMILARITY).		

FT	CHAIN	315	424	CASPASE-2 SUBUNIT p12 (BY SIMILARITY).
FT	DOMAIN	7	96	CAD.
FT	ACT SITE	248	248	BY SIMILARITY.
FT	ACT SITE	291	291	BY SIMILARITY.
FT	VASSPLIC	1	7	Missing (in isoform ICH-1S).
FT	VASSPLIC	294	424	/FtId=VSP_000803.
FT	VASSPLIC	294	424	DETRGDVDORGRSDSPGCEESDANKENIKLRLTPRSD
FT	VASSPLIC	294	424	MICGYACILKGTGAARNRTKRGSMTYEALITTVAEPSRDTHVA
FT	VASSPLIC	294	424	DMLVKNRKQIKOREGYAPGFEPHRCXENSEVCSTLCRIYL
FT	VASSPLIC	294	424	PEGVYPR -> GVSJGHILPLPCCCHCCTCCSMRQISEMI
FT	VASSPLIC	294	424	REMAKNGQIPQAVRRVMQTRKKISSCVCLHAPI (in
FT	VASSPLIC	294	424	isoform ICH-1S).
FT	VASSPLIC	294	424	/FtId=VSP_000804.
SQ	SEQUENCE	424 AA;	47959 MM;	72281050B8B2F60 CRC64;
Query Match		24.6%;	Score 305;	DB 1; Length 424;
Best Local Similarity		31.5%;	Pred. No. 3.7e-17;	
Matches	86;	Conservative	51;	Mismatches 82; Indels 54; Gaps 10;
QY		1 MSNPRLSEEEKYDSGAAIALIILC-----VTKAREGSEDLDALHEMFRQLRFESTM	52	
Db		166 ISEPP-----GLAILLINIHSESEKDLEYRGSGVDCASELLEFFHLIGYQTIV	213	
QY		53 KDPFAHQFOEELKEFKQAISREDPVSCAFVLMAHREGFLKGEDEMVLLENLFELAL	112	
Db		214 FHDQSAEEHSASLEFRFSKLPD-HQVVDSC-IYALLSHVEGGVGVTDLGLQLQEAFLRF	271	
QY		113 NNKNQCALRAKPXYIIQA-CRGEQRDPG-EIVYGDELIVWVKDSP-----Q	157	
Db		272 DVANCPNLIKPKRMFIQA-CRGEDETRDGVDQRDKQE---RSDSPCESDANKENIKL	327	
QY		158 TIPTTYTDALHYSTVEGYIAVHHDDKGSGEFIGTIVDVETK-RKHITELLEVTBRMAL	215	
Db		328 RLPTSDMLICGYAALKGTAMRNTRKGSYIALTLTFVEAESRDLTHVADMLVKNRKIQ	367	
QY		216 ALVYEGSKARKTN-----PETOSTLRRLRYL	241	
Db		388 ---REGVAPGTEPHRCCKMSKEYCSITLCDLYL	416	
RESULT 4				
ID	ICE2_MOUSE	STANDARD;	PRT;	435 AA.
AC	P29594; O08737;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2			
OS	protein.)			
OS	CASP2 OR ICH1 OR NEDD2 OR NEDD-2.			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RX	MEDLINE=95047319; PubMed=7958843;			
RA	Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;			
RT	"Induction of apoptosis by the mouse Nedd2 gene, which encodes a			
RT	protein similar to the product of the Caenorhabditis elegans cell			
RT	death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";			
RL	Genes Dev. 8:1613-1626(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C3H/An;			
RX	MEDLINE=97190206; PubMed=9038361;			
RA	van de Crien M., Vandenabeele P., Declercq W., van den Brande L.,			
RA	van Looy G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,			
RA	Fiers W.;			
RT	"Characterization of seven murine caspase family members.";			
RT	FEBS Lett. 403:61-69(1997).			
RN	[3]			

```

RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92328780; PubMed=1378265;
RX Kumar S, Tomooka Y, Noda M;
RT "Identification of a set of genes with developmentally down-regulated
RL expression in the mouse brain.";
RL Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival. May be important in
CC multistep carcinogenesis.
CC -1- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -1- TISSUE SPECIFICITY: High level expression seen in the embryonic
CC CNS, liver, lung, kidney, small intestine, and hair follicles of
CC vibrissae. Moderate expression seen in the skin, oral mucosa,
CC skeletal muscle, submandibular gland and thymus. In the adult, it
CC is highly expressed in spleen, lung and kidney. Moderately in the
CC brain, heart, testis, liver. Low levels in the thymus, skeletal
CC muscle, ovary and gut.
CC -1- DEVELOPMENTAL STAGE: During embryonic development is highly
CC expressed in several types of mouse tissue undergoing high rates
CC of programmed cell death such as central nervous system and
CC kidney.
CC -1- FTM: THE NATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC -----
DR EMBL; D28482; BAA25876.1; ALT_INIT.
DR EMBL; Y13085; CAA73527.1; ALT_INIT.
DR HSSB; P42574; ICP3.
DR MEROPS; C14.006; -.
DR MGD; MGI:97295; Casp2.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00176; ILIABCEZYME.
DR SMART; SMO0114; CARD; 1.
DR SMART; SMO0115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 152
FT CHAIN 1 152 BY SIMILARITY.
FT FT 153 316 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
FT CHAIN 317 435 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
FT FT 331 435 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
FT CHAIN 15 103 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
FT DOMAIN 15 103 CARD.
FT ACT_SITE 260 260 BY SIMILARITY.
FT ACT_SITE 303 303 BY SIMILARITY.
FT MUTAGEN 303 303 C->G: LOSS OF FUNCTION.
FT CONFLICT 71 71 MISSING (IN REF. 1).
SQ SEQUENCE 435 AA; 48896 MW; 898456AA76E7A676 CRC64;

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QY      29 REGGEEDLADLEHNERQRLREPSIMKRPPTAFQPEEELFKQQAIDSRDEPVSQAFVWLMA      88
Db      202 RSGGDVHTTLVTLVFKLLGVVHVLHQTAQEMQEKLONFQAQ-LIPAIRVTDSCV-VALLS      259
QY      89 HGREBGLKGEDEGWKLENTFEALNNKKCALRAKPEVYVYIIOACRGQRDPG-----140
Db      260 HGVGGVIGYVDKLLQGVFPRLEFDNANCSSLQNKPEKMFLLQACRGDETRGVQDQDGN      319
QY      141 -----ETVGGDEIVWVTKDSPQITPTVTDALHVSTVEGYIAYVHDQKSCFIOTLV      159
Db      320 HTSPGCGEESDADKEELMKMR-----LFTSDMIGVAGLCIKGNAMAMNTRGSGYIALT      374
QY      193 DVFLTKR-KHILIELLEVYRMAEALVEVGARAKTN-----PIQSTLKRRLYL      241
Db      375 QVSEPRACDMHVDMLVKVNAALKE-----REGVAPGTEPRCKREMSHYCSTLQGVYL      428

RESULT 5
ICE2 HUMAN
ID _ICE2_HUMAN STANDARD; PRT; 435 AA.
AC P42575; P42576;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (BC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1/1S).
GN CASP2 OR ICH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Petal brain;
RX MEDLINE=94373811; PubMed=8087842;
RA Weng L., Miura M., Bergeron L., Zhu H., Yuan J.;
RT "Ich-1, an Ice/ced-3-related gene, encodes both positive and negative
RL regulators of programmed cell death.";
RN Cell 78:739-750 (1994).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-155; ALA-161 AND
RA GLY-424.
RN [4]
RP Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RN Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Doebber A., Martinka S., Maupin R.;
RN Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
[4]
RP CLEAVAGE SITES.
RX MEDLINE=96206041; PubMed=8654923;
RA Xue D., Shaham S., Horvitz H.R.;
RT "The Caenorhabditis elegans cell-death protein CED-3 is a cysteine
RP protease with substrate specificities similar to those of the human
RL Cpp32 protease.";
RN Genes Dev. 10:1073-1083 (1996).
[5]
RP FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival.
CC -1- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Isoforms differ in the N- and C-termini;
CC Name=ICH-1L;
CC IsoId=P42575-1; Sequence=Displayed;
CC Note=Acts as a positive regulator of apoptosis;
CC Name=ICH-1S;
CC IsoId=P42575-2; Sequence=VSP_000801, VSP_000802;
CC Note=Acts as a negative regulator of apoptosis;

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CC -1- TISSUE SPECIFICITY: Expressed in larger amounts in the embryonic
CC lung, liver and kidney than in the heart and brain. In the adults
CC higher level expression is seen in the placenta, lung, kidney,
CC pancreas than in the heart, brain, liver and skeletal muscle.
CC -1- PFM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U13021; AA58959.1; -;
CC EMBL; U13022; AA58960.1; -;
CC EMBL; AY219042; AA025653.1; -;
CC EMBL; AC073342; AAP2346.1; -;
CC PIR; A54821; A54821.
CC HSSP; P29466; 1ICE.
CC MEROPS; C14.006; -;
CC Genew; HGNC:1503; CASP2.
CC MIM; 600639; -;
CC GO; GO:0004202; F.caspase-2 activity; TAS.
CC GO; GO:001899; F.enzyme binding; ISS.
CC GO; GO:0008632; P.apoptotic program; TAS.
CC GO; GO:0006508; P.proteolysis and peptidolysis; TAS.
CC InterPro; IPR001315; CARD.
CC InterPro; IPR002138; ICE p10.
CC InterPro; IPR001309; ICE p20.
CC InterPro; IPR002398; Peptidase_C14.
CC Pfam; PF00619; CARD; 1.
CC Pfam; PF00656; Peptidase_C14; 1.
CC PRINTS; PR00376; IL1BENZYM.
CC SMART; SM00114; CARD; 1.
CC SMART; SM00115; CASG; 1.
CC PROSITE; PS50209; CARD; 1.
CC PROSITE; PS01122; CASPASE_CYS; 1.
CC PROSITE; PS01121; CASPASE_HIS; 1.
CC PROSITE; PS50207; CASPASE_P10; 1.
CC PROSITE; PS50208; CASPASE_P20; 1.
CC K0 Hydroxylase; Thiol protease; Apoptosis; Zymogen; Polymorphism;
KW Alternative splicing
FT PROPEP 1 152
FT CHAIN 153 308 CASPASE-2 SUBUNIT P18.
FT PROPEP 309 316
FT CHAIN 317 435 CASPASE-2 SUBUNIT P13.
FT CHAIN 331 435 CASPASE-2 SUBUNIT P12.
FT DOMAIN 15 103 CARD.
FT ACT_SITE 260 260 BY SIMILARITY.
FT ACT_SITE 303 303 BY SIMILARITY.
FT VARSPIC 1 14 Missing (in isoform ICH-1S).
FT VARSPIC 306 435 /FTid=VSP_000801.
FT DETRGVDDGKXNHSAPGCEESDAGEKLPKRLPTRSD
FT MCGYACIKGTAAKNTKRGWYIEALQVSEKACMNVHVA
FT DMUYKVALIKDREGVAPGTFEHHCKEMSEVCTLCRLHYL
FT FPGHPPT -> GAIGISLGHLLFTAAATASAL (in
FT isoform ICH-1S).
FT /FTid=VSP_000802.
FT V -> L.
FT /FTid=VSP_016334.
FT P -> A.
FT /FTid=VAR_016335.
FT R -> G.
FT /FTid=VAR_016336.
FT C -> S; LOSS OF FUNCTION.
FT A -> T; LOSS OF FUNCTION.
FT MUTAGEN 303 303
FT MUTAGEN 352 A->T; LOSS OF FUNCTION.
FT SEQUENCE 435 AA; 48855 MW; 1652BC73F6286FB7 CRC64;
Query Match 23.3%; Score 289; DB 1; Length 435;

Best Local Similarity 31.1%; Pred. No. 7.3e-16;
Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;
QY 29 REGSEEDLDALHMFROLPRESTKRPPTAQPQBELEKPOQALDSKEDPVSQAFVYMA 88
Db 202 RSGDVPDSTLVTLVFKLIGYDVHVLCDQTAEMERKQNFQAQ-IPARVTDSC-IVALLS 259
QY 89 HGRGFLKGEHGVNWKLENFELALNNKCCALRAKPKVYIIQACRGEQDPG----- 140
Db 260 HGVGATYGVGDKLLQLOEVFQLPDNANCPSELQNKPKRFIQACRGDSDTDGVDQDGN 319
QY 141 -----ETVSGDEHIVWIKDSQTLPTTADALHVSTVEGYIAYRHDQKSCRTQTLV 192
Db 320 HAGSGCESDAGK-----KLPPKRLPTRSDMTCGVACTKGTAMRMTKGSWYIEALA 374
QY 193 DVFTKR--KGHLELITVTRMAELVQSKARKTN-----PEQSTLRKRYL 241
Db 375 QVFSERACDMHVAIDLKVNALIKD-----RGGYAGTEFHRCKEMSEVCTLCRLHYL 428
RESULT 6
ID ICE3 RAT STANDARD; PRT: 277 AA.
AC P55213; P70543; P97699; Q62993;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (SREBP cleavage activity 1)
DE (SCA-1) (LICE) (TRP).
GN CASP3 OR CPP32.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=101116;
RN [1]
RP MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling interleukin-1 beta converting enzyme
RT and CED-3.";
RL Oncogene 13:749-755 (1996).
RN [2]
RP SEQUENCE OF 30-241 FROM N.A.
RC MEDLINE=96042508; PubMed=7588240;
RX Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
RA Hirschfield A.N., Tilly J.L.;
RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
RT endonuclease activity from morphological apoptosis in granulosa cells
RT of the ovarian follicle.";
RL Endocrinology 136:5042-5053 (1995).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=97184204; PubMed=9030616;
RX Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
RA Roelcke P., Jr., Polier G.G., Paul S.M.;
RT "Cloning and expression of a rat brain interleukin-1beta-converting
RT enzyme (ICE)-related protease (IRP) and its possible role in
RT apoptosis of cultured cerebellar granule neurons.";
RL J. Neurosci. 17:1561-1569 (1997).
RN [4]
RP SEQUENCE OF 1-264 FROM N.A.
RA Yakovlev A.G.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory

```

CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
CC -1 SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (By similarity).
CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
CC -1 TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE
CC BUT NOT IN KIDNEY OR TESTIS.
CC -1 DEVELOPMENTAL STAGE: Highly expressed in neuron-enriched regions
CC of the developing brain, but down-regulated to low levels in the
CC adult brain.
CC -1 PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1 SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U49930; AAC52765.1; -
DR EMBL; U34685; AAC52261.1; -
DR EMBL; U84410; AAB41792.1; -
DR EMBL; U58656; AAB02722.1; -
DR PIR; I67437; I67437.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IILBENZIME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR KEMBL; Thiol protease; Zymogen; Apoptosis.
DR PROPEP; 1
DR PROPEP; 9
DR PROPEP; 10
DR PROPEP; 28
DR CHAIN; 29
DR CHAIN; 175
DR ACT SITE; 176
DR ACT SITE; 277
DR ACT SITE; 121
DR ACT SITE; 121
DR ACT SITE; 163
DR ACT SITE; 163
DR ACT SITE; 25
DR ACT SITE; 29
DR ACT SITE; 170
DR ACT SITE; 170
DR ACT SITE; 178
DR ACT SITE; 178
DR ACT SITE; 182
DR ACT SITE; 182
DR ACT SITE; 187
DR ACT SITE; 187
DR ACT SITE; 190
DR ACT SITE; 190
DR ACT SITE; 199
DR ACT SITE; 199
DR ACT SITE; 211
DR ACT SITE; 211
DR ACT SITE; 236
DR ACT SITE; 236
DR ACT SITE; 245
DR ACT SITE; 245
DR ACT SITE; 31491 MW; ADABP418E507402 CRC64;
DR ACT SITE; 277 AA;
DR ACT SITE; 22.6%; Score 279.5; DB 1; Length 277;
DR ACT SITE; Best local Similarity 32.8%; Pred. No. 2.4e-15;
DR ACT SITE; Matches 82; Conservative 35; Mismatches 106; Indels 27; Gaps 8;
DR ACT SITE; 9 EKVDMASAAALILICV-----KARSGSEEDIDALEHMFROJFESTIMKRPDTA 58
DR ACT SITE; 34 DSSIKMDYFENGLCTIINKNFKHSTGMSANGTVDVDAANIRFETFMALKYEVKKNKNDLTR 93
DR ACT SITE; 59 EQFOEELKFOQADISREDPVSCAFVVMHAGREGFLKGEDEGVKLENLFEALNNKQCQ 118

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DR Db 94 EIMELMNSVSEKEDHSKSSFFVC---VILSHGDEGVINGNP-VDLKLTSPFRGDYCR 149
DR Qy 119 ALRAKPKYIIQACRGEORDPG-ETVGGDEIYVWIKSDPQITPTTDAIHYSTVEGYIA 177
DR Db 150 SLTGPKFLFIQACGTGLDGCIEFDSDGDDMAC---QKIPVADFLYAYSTAPGYIS 205
DR Qy 178 YRHQKSGCFIOTLVDTYTKRKHILE--LITEVTRMA---EAEIVQSGARKTNP 230
DR Db 206 WRNSRDSGWFLOSLC-AMLKLYAHKLEFMHILTRVNRKVAIFESFSIDATTHAKQIFC 264
DR Qy 231 IOSTRKRLY 240
DR Db 265 IVSMULTKELY 274
DR RESULT 7
DR ICE3_CRIL0 STANDARD; PRT; 277 AA.
DR AC 060431;
DR DT 01-NOV-1997 (Rel. 35, Created)
DR DT 01-NOV-1997 (Rel. 35, Last sequence update)
DR DT 15-MAR-2004 (Rel. 43, Last annotation update)
DR DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DR DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DR DE (SCA-1)
DR GN CASP3 OR CPP32.
DR OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
DR OC Cricetulus.
DR OX NCBI_TaxID=10030;
DR RN [1]
DR RP SEQUENCE FROM N.A.
DR RC TISSUE=Brain;
DR RX MEDLINE=96183185; PubMed=8605870;
DR RA Wang X., Zielinski N.G., Yang J., Sakai J., Brown M.S.,
DR RA Goldstein J.L.;
DR RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
DR RT CPP32 during apoptosis."
DR RL EMO J. 15:1012-1020(1996).
DR CC -1 FUNCTION: Involved in the activation cascade of caspases
DR CC responsible for apoptosis execution. At the onset of apoptosis it
DR CC polythetically cleaves poly(ADP-ribose) polymerase (PARP) at a
DR CC 216-Asp|-Gly-217 bond. Cleaves and activates sterol regulatory
DR CC element binding proteins (SREBPs) between the basic helix-loop-
DR CC helix leucine zipper domain and the membrane attachment domain.
DR CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
DR CC -1 SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
DR CC (By similarity).
DR CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
DR CC -1 PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
DR CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
DR CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
DR CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
DR CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
DR CC VICE VERSA (BY SIMILARITY).
DR CC -1 SIMILARITY: Belongs to peptidase family C14.
DR CC -----
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DR CC -----
DR EMBL; U27463; AAB01511.1; -
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.

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PRINTS: PR00376; IILBCENZME.
 DR SMART: SMO0115; CASG: 1.
 DR PROSITE; PS01122; CASPASE_CYS: 1.
 DR PROSITE; PS01121; CASPASE_HIS: 1.
 DR PROSITE; PS50207; CASPASE_P10: 1.
 DR PROSITE; PS50208; CASPASE_P20: 1.
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
 FT PROPEP 1 9
 FT PROPEP 10 28
 FT CHAIN 29 175
 FT CHAIN 176 277
 FT ACT SITE 121 121
 FT ACT SITE 163 163
 FT SEQUENCE 277 AA; 31612 MW; 0BF3A4590A2828A3 CRC64;
 Query Match 22.4%; Score 277.5; DB 1; Length 277;
 Best Local Similarity 35.9%; Pred. No. 3,4e-15;
 Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;
 QY REGSEDDDALEHMFROIRFESTMKRDPFAEQFOELEKFOQALDSREDPVSCAFVDMA 88
 DB 64 RSGTVDAKAKETMTALKYEVKKNKDLTREIVELMKAKSKEDSKSSFC--VILS 120
 QY HGRSEGLKGEDEGEVYLTENLFEALNNKNCQALRAKPKVYIIQACRGEQDPG-ETVGGDE 147
 DB 121 HDEGVITPFTDGP-IDLKLTLYFRDGYCRSLIGKPKFLIIQACRGTEIDCGIETDSGTE 179
 QY 148 IYMWIKDSPTPTPTDIAHYSTVEGYIAYRHDKGSGFIOIYDVFKRGHILE--- 204
 DB 180 DDMTC---QKIPVEADFLYAVSTAGYYSWRPKDGSWFISLSCML-KLVAHKLFEVH 234
 QY 205 ILTEVTRMA---EALVQEGKARKTNPEIOSTLEKRLY 240
 DB 235 ILRVNRKVAATERPESFSLDTPHAKQICIVSMILKELY 274

RESULT 8
 ICE3_MOUSE STANDARD; PRT; 277 AA.
 AC P70677; 008668; 09QW14;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1) (LICE).
 GN CASP3 OR CPP32.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96358624; PubMed=8761296;
 RA Juan T.S.-C., McNiece I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
 RA Fletcher F.A.;
 RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
 RT a cysteine protease resembling interleukin-1 beta converting enzyme
 RT and CBD-3.";
 RL Oncogene 13:749-755 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97224429; PubMed=9070890;
 RA Mukasa T., Utase K., Momoi M.Y., Kimura I., Momoi T.;
 RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
 RT activation of CPP32 in the apoptosis induced by a withdrawal of
 RT NGF.";
 RL Biochem. Biophys. Res. Commun. 231:770-774 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9038361;
 RA van de Craen M., Vandenberghe P., Declercq W., van den Brande I.,

RA van Loo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RL FEBS Lett. 403:61-69 (1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC Tissue=Brain;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; Tissue=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smailus D.E.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.);
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE OF 58-277 FROM N.A.
 RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
 RA Fortin J.-P., Sekaly R.-P.;
 RT Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RL [1-] FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9 (by similarity).
 CC cleaves IL-1 beta between an Asp and an Ala, releasing the mature
 CC cytokine which is involved in a variety of inflammatory processes.
 CC [1-] SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC [1-] SUBCELLULAR LOCATION: Cytoplasmic.
 CC [1-] TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
 CC kidney and heart. Lower expression in brain, skeletal muscle and
 CC testis.
 CC [1-] PTM: CLEAVAGE BY GRANTYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).
 CC [1-] SIMILARITY: Belongs to peptidase family C14.
 CC
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 CC
 CC EMBL; U54803; AAC52768.1; JOINED.
 CC EMBL; U54802; AAC52768.1; JOINED.
 CC EMBL; U49929; AAC52764.1; -.

	Query Match	22.1%	Score 273.5	DB 1	Length 277
	Best Local Similarity	34.8%	Pred. No. 7.2e-15		
	Matches 77	Conservative 34	Mismatches 93	Indels 17	Gaps 7
QY	28	ARSESSEDLDLLEIMFROLFRESIMKRPPTAEQOELEHKEQOALDSSEDPVSCAFVLLM	87		
Db	63	SRSGTDVDAANLRTFMGLKYQVANKNDLTREDLLEMDYSKEDHSRSSSEFVC---VIL	119		
QY	88	AHGEGLKGEDEGDMVTKLETFEALNNKNCQALRAKRPVYIIIOACRGQRDPG-ETVSGD	146		
Db	120	SHGEGVYGTNG-VELKLTSPFRPDYCSLTGKEXPLFIIOACRGTELDGILEDSGT	178		
QY	147	EIVWVAKDSFQITPTTYTDALHVSVEVGEIAYLRDQKSCSCITQTLVDFTRKGHILE--	204		
Db	179	DEMAC---OKIPVEADFLVAYASTAGYYSWNRKSDGSMWISQSLCML-KLYAHKLEFM	233		
QY	205	-LITETVTRMA---EAEIVQSGKARPTNEIGSTLAKRLY	240		
Db	234	HILTRVNRKVNATFEESFSLDSTHAKQOITCVISMTLKEIY	274		

OK NCBI_TaxID=9606;
 RP [1] SEQUENCE FROM N.A., AND VARIANT GLUT-190.
 RC TISSUE=T-cell;
 RX MEDLINE=95074098; PubMed=7983002;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RT "CPP3, a novel human apoptotic protein with homology to
 RL Caenorhabditis elegans cell death protein Ced-3 and mammalian
 j. Biol. Chem. 269:30761-30764(1994)."
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=95292347; PubMed=7774019;
 RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
 RA Beidler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;
 RT "Kappa/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitab
 RL protease that cleaves the death substrate poly(ADP-ribose)
 j. Cell 81:801-809(1995)."
 RN [3]
 RN SEQUENCE FROM N.A.
 RA Vallette F.M., Oliver L.J.;
 RT "Control of the activation of the procaspase-3 by a sequence located
 RL at the N-terminus of the p17 subunit.";
 RN Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A., AND VARIANT GLUT-190.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Foel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witzak L.A., Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A., AND VARIANT GLUT-190.
 RC TISSUE=Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg K.S., Bietlow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.C., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millhys S.J.,
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Ricardus S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.C.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Scherter A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RL human and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RN SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
 RP MEDLINE=95319529; PubMed=7956430;
 RX Nicholson D.W., Ali A., Thornberry N.A., Vaillancourt J.P., Ding C.K.,
 RA Gulland M., Gareau Y., Griffin P.R., Labelle M., Lazebnik Y.A.,
 RA Munday N.A., Raju S.M., Smolton M.E., Yamin T.-T., Li V.L.,
 RA Miller D.K.;
 RT "Identification and inhibition of the ICE/CED-3 protease necessary
 RL for mammalian apoptosis.";
 RN Nature 376:37-43(1995).
 RN [7]
 RN X-RAY CRYSTALOGRAPHY (2.5 ANGSTROMS) OF 28-277.
 RX MEDLINE=96266352; PubMed=8673666;
 RA Rotonda J., Nicholson D.W., Fazil K.M., Gallant M., Gareau Y.,
 RA Labelle M., Peterson E.P., Rasper D.M., Ruel R., Vaillancourt J.P.,
 RA Thornberry N.A., Becker J.W.;
 RT "The three-dimensional structure of apopain/CPP32, a key mediator of
 RL apoptosis.";

RL Nat. Struct. Biol. 3:619-625 (1996).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
 RX MEDLINE=97197830; PubMed=9045680;
 RA Mittl P.R.E., di Marco S., Krebs J.F., Bai X., Katanewsky D.S.,
 RA Priestle J.P., Tomasselli K.J., Grueter M.G.;
 RT "Structure of recombinant human CPP32 in complex with the
 RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone";
 RL J. Biol. Chem. 272:6539-6547 (1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
 RX MEDLINE=20283632; PubMed=10821855;
 RA Lee D., Long S.A., Adams U.L., Chan G., Vaidya K.S., Francis T.A.,
 RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
 RA Levy M.A., Dewolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
 RA Ryan M.D., Hattiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
 RA Johnson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
 RA Jack M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
 RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
 RT inhibit apoptosis and maintain cell functionality";
 RL J. Biol. Chem. 275:16007-16014 (2000).
 RN [10]
 RP PROCESSING.
 RX MEDLINE=96353838; PubMed=8755496;
 RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
 RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomasselli K.J.,
 RA Litwack G., Alnemri E.S.;
 RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
 RT apoptotic cysteine protease containing two FADD-like domains";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469 (1996).
 RN [11]
 RP CLEAVAGE OF HUNTINGTIN.
 RX MEDLINE=96331285; PubMed=8696339;
 RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
 RA Graham R.K., Brom M., Kazemi-Esfarjani P., Thornberry N.A.,
 RA Vallancourt J.P., Hayden M.R.;
 RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
 RT is modulated by the polyglutamine tract";
 RL Nat. Genet. 13:442-449 (1996).
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-1-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9. Involved in the
 CC cleavage of huntingtin.
 CC -1- ENZYME REGULATION: Inhibited by isatin sulfonamides.
 CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
 CC and kidney. Moderate levels in brain and skeletal muscle, and low
 CC in testis. Also found in many cell lines, highest expression in
 CC cells of the immune system.
 CC -1- PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
 CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
 CC PROPERTIES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
 CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
 CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
 CC AND VICE VERSA.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC
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 CC -----
 CC EMBL: U13737; AAA65015.1; -
 CC DR EMBL: U13738; AAB60355.1; -
 CC DR EMBL: U26943; AAA74929.1; -
 CC DR

DR EMBL: A1413269; CAC88866.1; -
 DR EMBL: AY199866; AA025654.1; -
 DR EMBL: BC016926; AAL16926.1; -
 DR EIR: A53315; A53315.
 DR PIR: 1PAU; 07-JUL-97.
 DR PDB: 1CP3; 24-DEC-97.
 DR PDB: 1GFN; 23-JUN-00.
 DR MEROPS: C14.003; -
 DR Genew: HANC:1504; CASP3.
 DR MIM: 600636; -
 DR GO: GO:0004208; F:caspase-3 activity; TAS.
 DR GO: GO:0008624; P:induction of apoptosis by extracellular sig. .; TAS.
 DR GO: GO:0008629; P:induction of apoptosis by intracellular sig. .; TAS.
 DR GO: GO:0009405; P:pathogenesis; TAS.
 DR InterPro: IPR002138; ICE_p10.
 DR InterPro: IPR001398; ICE_p20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; IL1BCENZYM.
 DR SMART: SM00115; CASc; 1.
 DR PROSITE: PS01122; CASPASE_CYS; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR Hydrolase: Thiol protease; Zymogen; Apoptosis; Polymorphism;
 KW 3D-structure. 1 9
 FT PROPEP 1 28
 FT PROPEP 10 9
 FT CHAIN 29 175
 FT CHAIN 176 277
 FT ACT_SITE 121 121
 FT ACT_SITE 163 163
 FT VARIANT 190 190
 FT FT 31 36
 FT CONFLICT 31 36
 FT STRAND 36 36
 FT STRAND 43 51
 FT HELIX 57 59
 FT TURN 60 60
 FT TURN 65 66
 FT TURN 67 80
 FT HELIX 81 82
 FT TURN 81 82
 Query Match 22.0%; Score 272.5; DB 1; Length 277;
 Best Local Similarity 31.9%; Pred. No. 8,7e-15;
 Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;
 QY 9 EEEKYDMSGALALILCVTK-----ARSGSEEDLALHEMFEROLRESMKRPTA 58
 DB 34 DSYGYKMDPEMGCIITNNNGHFKSTGTSRSGTVDVDAIMREFRMLKYEVNRKNDITR 93
 QY 59 EGFQEELEKQQAIDSRDEYSCAFVYLMHGRGELKGDG--EWYKLELFPALNNKN 116
 DB 94 EEIYELMRDVSKEHDSRSSFEVC--VLSHGERGIIFGTNGPYDLKKTINF--RGDR 147
 QY 117 GQALRAKPKYIITDAGCEGDEPDG--ETVYGDEIYVVIKDSFQITPTYTDAIHYVSTVEGY 175
 DB 148 CRSLTGKPKFIIDACGTBIDSGIFRIDSVDDMAC---HKIPVADFLVASTAPGY 203
 QY 176 IAYRHDKSGSCFIOTLVDFTK--RKSHIELLETVTRRNA--EELVYO--EGARKTNP 229
 DB 204 YSWNSNDGSGWFIISLCMKLEKQYADKLEFMHILTRVVRKVAITEFESFSPDATHAKQIP 263
 QY 230 EIGSTLKKRLY 240
 DB 264 CIVSMLTRELY 274
 RESULT 10
 ICE7 MOUSE STANDARD; PRT; 303 AA.
 ID ICE7 MOUSE
 AC P97864; 008669;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (rel. 35, last sequence update)
DT 10-OCT-2003 (rel. 42, last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine protease) (Apoptotic
DE protease Mch-3).
GN CASP7 OR MCH3 OR LICE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
KN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., Mchiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
RL Genomics 40:86-93 (1997).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khorojy Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Mortaminin enhances CPP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid.";
RL Biochem. Biophys. Res. Commun. 232:192-197 (1997).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,
RA Piers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69 (1997).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.D., Ushin T.B., Toshiyuki S., Carninci P., Schaefer T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McManus P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves and activates sterol
CC promotes programmed cell death (by similarity). Overexpression
CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC KIDNEY, LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -1- PM: CLEAVAGES BY GRANTYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).

CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC -----
DR EMBL: U67321; AAC53068.1; ALT_INIT.
DR EMBL: D86353; BAA19730.1; -.
DR EMBL: Y13088; CAA73530.1; -.
DR EMBL: BC005428; AAH05428.1; -.
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.004; -.
DR MCD: MGI:109383; Casp7.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILBCENZYM.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23
FT CHAIN 24 198
FT PROPEP 199 206
FT CHAIN 207 303
FT ACT_SITE 144 144
FT ACT_SITE 186 186
FT CONFLICT 10 11
FT CONFLICT 45 45
FT CONFLICT 48 49
SQ SEQUENCE 303 AA; 34060 MW; 7477875BDE5F744 CRC64;
Query Match 21.8%; Score 270; DB 1; Length 303;
Best Local Similarity 32.6%; Pred. No. 1.5e-14;
Matches 71; Conservative 36; Mismatches 101; Indels 10; Gaps 4;
QY 29 RCSEBDDALAHMFRQCFEFESTMKRDPFAEQFOEHLERFOQALDSREDPVSQAFVWMA 88
DB 87 RRGTKDAGALFKPCFQNLGFVTVHNDSCAMQDLRASEBDDHNS---ACFAVLIS 143
QY 89 HREBEPKGEDEAMKLENTLPEALNNKQCALPAPKVTYIIOACRGEQDPGETVGDEI 148
DB 144 HEEEDLLYKQDG-VPIPIDLNAHFRGDRCKTLLKPKLFFIOACHRGTELDGDIGQADSGPI 202
QY 149 VVWIKDSFQITPTTYDALHVVSTVEGYAYRHDOGSGCIQTLTVVFTK--RKHILELL 206
DB 203 NDIDANPNPKIPEVADFLFAVSTVPGYISWRPGKGSWFVQALCSILNEHGDLBIMQTL 262
QY 207 TEVTRPMAEALIVDEGKAR---KTNPEIQSTLRKELY 240
DB 263 TRVDNRVARHRESQSDDPFNEKQIIPCMVSLTRELY 300
RESULT 11
ICE7_MESAU
ID ICE7_MESAU STANDARD; PRT; 303 AA.
AC P55214;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
DE (ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity 2)
DE (SCA-2).
GN CASP7 OR MCH3.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=Syrian; TISSUE=Liver;
 RX MEDLINE=96224303; PubMed=8643593;
 RA Pal J., Brown M.S., Goldstein J.L.;
 RT "Purification and cDNA cloning of a second regulatory element binding
 protease that cleaves and activates sterol regulatory element binding
 proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 responsible for apoptosis execution. Cleaves and activates sterol
 regulatory element binding proteins (SREBPs). Proteolytically
 cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
 bond. Overexpression promotes programmed cell death (By
 similarity).
 CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PTM: CLEAVAGES BY GAZZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
 SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
 CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
 VICE VERSA (By similarity).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U47332; AAC52595.1; -
 DR HSSP: P42574; 1PAU.
 DR MEROPS: C14.004; -
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; Peptidase C14.
 DR Pfam: PF00656; Peptidase C14; 1.
 DR PRINTS: PR00376; IILBENZYM.
 DR SMART: SM0115; CASC; 1.
 DR PROSITE: PS01122; CASPASE_C14; 1.
 DR PROSITE: PS01121; CASPASE_HIS; 1.
 DR PROSITE: PS50207; CASPASE_P10; 1.
 DR PROSITE: PS50208; CASPASE_P20; 1.
 DR HydroLase; Thiol protease; Zymogen; Apoptosis.
 KW PROPEP 1 23
 FT CHAIN 1 198 CASPASE-7 SUBUNIT P20.
 FT PROPEP 199 206 BY SIMILARITY.
 FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
 FT ACT_SITE 144 144 BY SIMILARITY.
 FT ACT_SITE 186 186 BY SIMILARITY.
 FT ACT_SITE 303 AA; 34037 MW; EA29356D90984648 CRC64;
 SQ SEQUENCE

Query Match 21.0%; Score 260; DB 1; Length 303;
 Best Local Similarity 31.7%; Pred. No. 9, 8e-14;
 Matches 69; Conservative 39; Mismatches 100; Indels 10; Gaps 5;

OY 29 RCGSEDDALHEMFQRLFESESTMKRDPFAEQFOELEKFOALISREDDPVACAFVWMA 88
 DB 87 RKGTDADALFECFSLGFDVVVNDSCAKKQDLIRKASEDHNS--ACFACVLLS 143
 OY 89 HREREGKCGDGVNLENIFFALNNKNCQALRANKYVITQACRGEQDPPGTTGSDGI 148
 DB 144 HGEENITLTKDG-VITIKDITAFHRGDRCKTLEKFKLFFIQCRGTELDGQVADSGPI 202
 OY 149 VWVTKDSPQITPTTALAHVSTVEGTAIVRHQDKSCFQITLVVFTK-RKCHILELL 206
 DB 203 NEIDNAPRKXIPLEADFLFAYSTVPGYVSWNPGKSWFQALCSILDEHGKOLEITWQIL 262

OY 207 TEVTRMA--BAEIVOE-GKARKNPEIQSTLRKLY 240
 DB 263 TRVNDRAHAFESQCDPCFNEKKQIPCMVSMILTKELY 300

RESULT 12
 ICE7_HUMAN STANDARD; PRT; 303 AA.
 ID P55210; Q13364; Q96BA0;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
 DE (ICE-LAP3) (Apoptotic protease Mch-3) (CMT-1).
 GN CASP7 OR MCH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=96139498; PubMed=8576161;
 RA Duan H., Chinaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
 RA Dixit V.M.;
 RT "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
 cell death protein Ced-3 is activated during Fas- and tumor necrosis
 factor-induced apoptosis.";
 RL J. Biol. Chem. 271:1621-1625(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Spleen;
 RX MEDLINE=96147144; PubMed=8567622;
 RA Lippe J.A., Gu Y., Sarnacki C., Caron P.R., Su M.S.-S.;
 RT "Identification and characterization of CPP32/Mch2 homolog 1, a novel
 cysteine protease similar to CPP32.";
 RL J. Biol. Chem. 271:1825-1828(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=F-cell;
 RX MEDLINE=96105019; PubMed=8521391;
 RA Fernandez-Alnemir T., Takahashi A., Armstrong R.C., Krebs J.,
 RA Fritz L.C., Tomaselli K.J., Wang L., Yu Z., Croce C.M., Salvesson G.,
 RA Earnshaw W.C., Litwack G., Alnemir E.S.;
 RT "Mch3, a novel human apoptotic cysteine protease highly related to
 CPP32.";
 RL Cancer Res. 55:6045-6052(1995).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND ALPHA').
 RC TISSUE=Fetal lung, and Fetal spleen;
 RX MEDLINE=97224489; PubMed=9070923;
 RA Uyan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Fletcher F.A.;
 RT "Identification and mapping of Casp7, a cysteine protease resembling
 CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
 RL Genomics 40:86-93(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Skin;
 RX MEDLINE=2238257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Mullany S.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RT "The C. elegans cell death gene ced-3 encodes a protein similar to
 RT mammalian interleukin-1 beta-converting enzyme.";
 RT Cell 75:641-652(1993).
 RN [2]
 RP REVISION TO 418.
 RA Horvitz H.R.;
 RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Burton J.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Dublin R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Acts as a cysteine protease in controlling programmed
 CC cell death by proteolytically activating or inactivating a
 CC substrate protein or proteins, a potential substrate may be ced-4.
 CC Alternatively it might directly cause cell death by
 CC proteolytically cleaving proteins that are crucial for cell
 CC viability.
 CC -1- SUBUNIT: Could be a heterodimer of two subunits derived from the
 CC precursor sequence by a probable autocatalytic mechanism.
 CC -1- DEVELOPMENTAL STAGE: Most abundant during embryogenesis and is
 CC also detected at later stages.
 CC -1- PTM: May be regulated by phosphorylation.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 1 CARD domain.
 CC -----
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 CC -----
 DR EMBL: L29052; AAA27982.2; -;
 DR EMBL: AF210702; AAG42045.1; -;
 DR EMBL: Z81049; CAB61001.2; -;
 DR PIR: A49429; A49429.
 DR HSSP: P42574; 1CP3.
 DR MEROPS: C14.002; -;
 DR WormBep: C4BD1.2; CE29088.
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS: PR00376; ILBCEZYME.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00115; CASC; 1.
 DR PROSITE: PSS0209; CARD; 1.
 DR PROSITE: PSS01122; CASPASE_CYS; 1.
 DR PROSITE: PSS01121; CASPASE_HIS; 1.
 DR PROSITE: PSS0207; CASPASE_P10; 1.
 DR PROSITE: PSS0208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.
 KW CELL DEATH PROTEIN 3 SUBUNIT 1
 FT CHAIN 1 371
 FT
 FT CHAIN 372 503
 FT
 FT DOMAIN 1 91
 FT DOMAIN 107 205
 FT ACT_SITE 304 304
 FT ACT_SITE 358 358
 FT MUTAGEN 27 27
 FT MUTAGEN 65 65
 FT MUTAGEN 360 360
 FT MUTAGEN 449 449
 FT MUTAGEN 466 466
 A->V: IN N2430; LOSS OF FUNCTION.
 A->Y: IN N2430; LOSS OF FUNCTION.

FT MUTAGEN 483 483 E->K: IN N2426; LOSS OF FUNCTION.
 FT MUTAGEN 486 486 S->F: IN N1163; LOSS OF FUNCTION.
 SQ SEQUENCE 503 AA; 56616 MW; 722D5831F94AA69 CRC64;
 Query Match 20.1%; Score 248.5; DB 1; Length 503;
 Best Local Similarity 27.9%; Pred. No. 1.5e-12;
 Matches 68; Conservative 42; Mismatches 93; Indels 41; Gaps 6;
 QY 29 REGSEEDIDALEHMFROQLRFESTYKRDPTAQQFQEELEKPPQALDSRDPVSCAFVYMA 88
 Db 259 RRGTRADKNDLNTNFRGCGYVICKDNLTRGGMILITIDFAK---HSHGDSALVLIS 314
 QY 89 HGRGEGFLKGEDEGEMWKLLENLFEALNNKCOALRAKPYVYIIQACRGEORPDPEYV----- 143
 Db 315 HGEENVYIIQVDDIPSTHEITVDLNAANAPRLANPKYVFVQACGGERDNGFVLDSDV 374
 QY 144 -----GGDEIVWYIKDSP-----OTIPYTDALHYVSVGEYIAYR 179
 Db 375 GVPAFLRRGWND-----RDGPLNPLGCVRPQVQVWKKPSQADILAYATTAQYVSWR 429
 QY 180 HDQKSCSTIQTIVDYFT--KKKHILELTETVRMAEALVQEG-KARKTPETIOSTLR 236
 Db 430 NSRGSWEFIQAVCEVFSFHADMVDELTEVYKKAAGPQTSQGSNLIKQMPWMTSRL 489
 QY 237 KELY 240
 Db 490 KKFY 493
 RESULT 14
 IC3_DROME STANDARD; PRT; 339 AA.
 ID IC3_DROME
 AC 001382; Q9YAH1; 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase precursor (EC 3.4.22.-) (drice).
 GN ICB OR CG7788.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=97327558; PubMed=9184225;
 RA Fraser A.G., Evan G.I.;
 RT "Identification of a Drosophila melanogaster ICE/CED-3-related
 RT protease, drice".
 RL EMO J. 16:2805-2813(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Peiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck B.P., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Fodor C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasner K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Jatali M., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.N., Moy M., Murphy B., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spadling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S.-Y., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley; TISSUE=Head;
RC MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Garin H., Krommiller B., Pacleib J.M., Park S., Wan K.H.,
RA Rubin G.M., Celniker S.E.;
RT "A Drosophila full-length cDNA resource";
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Acts downstream of rpr.
CC Cleaves baculovirus p35 and lamn Dmo in vitro.
CC -1- SUBUNIT: Heterodimer of a 21 kDa (p21) and a 12 kDa (p12) subunit.
CC -1- DEVELOPMENTAL STAGE: Expressed at all stages where apoptosis
CC occurs.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC -----
DR EMBL; Y1261; CAA72937.1; -;
DR EMBL; AE003771; AAF5639.1; -;
DR EMBL; AY058451; AAL13680.1; -;
DR HSSP; P42574; 1PNU.
DR MEROPS; C14.015; -;
DR FLYBASE; FBgn0019972; Ice.
DR GO; GO:0004207; P:effector caspase activity; NAS.
DR GO; GO:0006915; P:apoptosis; NAS.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SMO0115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
DR Hydroxylase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 28 BY SIMILARITY.
FT CHAIN 29 217 CASPASE SUBUNIT P21 (BY SIMILARITY).
FT PROPEP 218 230 BY SIMILARITY.
FT CHAIN 231 339 CASPASE SUBUNIT P12 (BY SIMILARITY).
FT ACT_SITE 169 169 BY SIMILARITY.
FT ACT_SITE 211 211 BY SIMILARITY.
FT CONFLICT 151 151 A -> S (IN REF. 1).
FT CONFLICT 265 265 S -> T (IN REF. 1).
SQ SEQUENCE 339 AA; 37363 MM; E105ED29518507EC CXC64;

Query Match 20.0%; Score 247.5; DB 1; Length 339;
Beet local similarity 30.5%; Pred. No. 1,1e-12;
Matches 60; Conservative 42; Mismatches 76; Indels 19; Gaps 5;
Qy 27 KARGSEDDALDLMHMRQLRFPSTMTKRDPTAEPQSELEKFGQAIDSRDPVSCAFVYL 86
Db 110 KSRGVTVDENLIRLVKQDFEVTYKDC---RYKDIARTIEVAASQNHSDPCIIVAI 166
Qy 87 MAHGREFFLKGEDEMYKLENTFEALNNKQALRAKPKVYIIQACRGQRDPSETV--- 143
Db 167 LSHMEMYIYIAKQIQYKIDNIMSFYANRCPDSIAKPKKFFIQACQGRDLDDGVTVQRS 225
Qy 144 ---GGSEIYVWIKSDPQITPTDYDALHYSTVEGYIAYRHDKSCFCIOTLVDFVTK-- 197
Db 226 QETEDGD-----SSMYKIPVHADFLIAYSTVGFYSWNTTSGSNFMQSLCAELANG 279
Qy 198 RKGHILELLFEVTRRMA 214
Db 280 KRDLITLTLFVCGQVA 296
RESULT 15
ICE8 HUMAN STANDARD; PRT; 479 AA.
AC Q14790; Q14676; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796;
AC Q15780; Q15806; Q8TD11; Q8TD12; Q8TD13; Q8TD14; Q8TD15; Q96T22;
AC Q9C084; Q9U081;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-8 precursor (BC 3.4.22.-) (ICE-1-like apoptotic protease 5)
DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-
DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
DE (Apoptotic protease Mch-5) (CASP4).
GN CASP8 OR MCH5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 5; 6; 7 AND 8).
RX TISSUE=B-cell, and thymus;
RC MEDLINE=96279826; PubMed=8681376;
RA Boldin M.P., Goncharov T.M., Golitsev Y.V., Wallach D.;
RT "Involvement of MACH, a novel MORT1/FADD-interacting protease, in
RT Fas/Apo-1- and TNF receptor-induced cell death.";
RL Cell 85:803-815(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RX MEDLINE=96279827; PubMed=8681377;
RA Muzio M., Chinnaiyan A.M., Kischkel F.C., O'Rourke K., Shevchenko A.,
RA Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann M.,
RA Krammer P.H., Peter M.E., Dixit V.M.;
RT "FLICE, a novel FADD-homologous ICE/CED-3-like protease, is recruited
RT to the CD95 (Fas/Apo-1) death-inducing signaling complex.";
RL Cell 85:817-827(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RC TISSUE=T-cell;
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandez-Alnemri T., Armstrong R.C., Krebe J.F., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaselli K.J.,
RA Litwack G., Alnemri E.S.;
RT "In vitro activation of CPP32 and Mch3 by Mch4, a novel human
RT apoptotic cysteine protease containing two FADD-like domains";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132295; PubMed=9931493;
RA Grenet J., Teitz T., Wei T., Valentine V., Kidd V.J.;
RT "Structure and chromosome localization of the human CASP8 gene";
RL Gene 226:225-232(1999).

[5]
SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=97375543; PubMed=9228018;
RA Srinivasula S.M., Ahmad M., O'Conne S., Bullrich F., Banks S.,
RA Fernandes-Alnemri T., Croce C.M., Litwack G., Tomasselli K.J.,
RA Armstrong R.C., Alnemri E.S.,
RA "FAME-1, a novel FADD-like anti-apoptotic molecule that regulates
RT Fas/TNFR1-induced apoptosis.";
RL J. Biol. Chem. 272:18542-18545 (1997).
[6]
SEQUENCE FROM N.A.
MEDLINE=21100893; PubMed=1161814;
RA Hadano S., Yamagisawa Y., Skaug U., Fichter K., Nasir J.,
RA Martindale D., Koop B.F., Scherer S.W., Nicholson D.W., Rouleau G.A.,
RA Ikeda J.-E., Hayden M.R.,
RT "Cloning and characterization of three novel genes, A152CR1, A152CR2,
RT and A152CR3, in the juvenile amyotrophic lateral sclerosis (ALS2)
RT critical region at chromosome 2q33-q34: candidate genes for ALS2.";
RL Genomics 71:200-213 (2001).
[7]
SEQUENCE FROM N.A. (ISOFORM 7), AND FUNCTION OF ISOFORM 7.
TISSUE=Leukocyte;
MEDLINE=22005982; PubMed=12010809;
RA Himeji D., Horinuchi T., Tsukamoto H., Hayashi K., Watanabe T.,
RA Harada M.,
RT "Characterization of caspase-8L: a novel isoform of caspase-8 that
RT behaves as an inhibitor of the caspase cascade.";
RL Blood 99:4070-4078 (2002).
[8]
SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 9), AND INTERACTION OF ISOFORM 9
WITH BCAP31 AT THE ENDOPLASMIC RETICULUM.
MEDLINE=21927603; PubMed=11917123;
RA Breckenridge D.G., Nguyen M., Kupzig S., Reith W., Shore G.C.,
RT "The procaspase-8 isoform, procaspase-8L, recruited to the BAP31
RT complex at the endoplasmic reticulum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4331-4336 (2002).
[9]
SEQUENCE FROM N.A. (ISOFORM 7).
TISSUE=Leukocyte;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Heaton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[10]
PARTIAL SEQUENCE, AND PROCESSING.
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RA Srinivasula S.M., Ahmad M., Fernandes-Alnemri T., Litwack G.,
RA Alnemri E.S.,
RT "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1
RT protease Mcb5 is a CrmA-inhibitable protease that activates multiple
RT Ced-3/ICE-1-like cysteine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491 (1996).
[11]
FUNCTION.
MEDLINE=97160607; PubMed=9006941;
RA Muzio M., Salvesen G.S., Dixit V.M.,
RT "FICE induced apoptosis in a cell-free system. Cleavage of caspase
RT zymogens.";
RL J. Biol. Chem. 272:2952-2956 (1997).
[12]
PROCESSING.
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RA Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M.,
RA Kramer P.H., Peter M.B.,
RT "FICE is activated by association with the C95 death-inducing
RT signaling complex (DISC)."
RL EMBO J. 16:2794-2804 (1997).
[13]
CHARACTERIZATION OF ISOFORM 7.
MEDLINE=20318377; PubMed=10860845;
RA Horinuchi T., Himeji D., Tsukamoto H., Harashima S., Hashimura C.,
RA Hayashi K.,
RT "Dominant expression of a novel splice variant of caspase-8 in human
RT peripheral blood lymphocytes.";
RL Biochem. Biophys. Res. Commun. 272:877-881 (2000).
[14]
INTERACTION WITH BCL2, BCL2L1 AND BCAP31.
MEDLINE=97477382; PubMed=9334338;
RA Ng F.W.H., Nguyen M., Kwan T., Branton P.E., Nicholson D.W.,
RA Cromlish J.A., Shore G.C.,
RT "p28 Bap31, a Bcl-2/Bcl-XL- and procaspase-8-associated protein in the
RT endoplasmic reticulum.";
RL J. Cell Biol. 139:327-338 (1997).
[15]
INTERACTION WITH PEAL5.
MEDLINE=99369240; PubMed=10442631;
RA Condorelli G., Vigliotta G., Cafieri A., Trencia A., Andalo P.,
RA Oriente F., Mele C., Carnio M., Fornisano F., Beggiato F.,
RT "PEB/PEA-15: an anti-apoptotic molecule that regulates Fas/TNFR1-
RT induced apoptosis.";
RL Oncogene 18:4409-4415 (1999).
[16]
X-RAY CRYSTALLOGRAPHY (2.8 ÅNGSTROMS).
MEDLINE=99451259; PubMed=10508784;
RA Blanchard H., Kodandapani L., Mittl P.R.E., Di Marco S., Krebs J.F.,
RA Wu J.C., Tomaselli K.J., Gnetter M.G.,
RT "The three-dimensional structure of caspase-8: an initiator enzyme in
RT apoptosis.";
RL Structure 7:1125-1133 (1999).
[17]
VARIANT CASP8D TRP-248.
MEDLINE=2239940; PubMed=12353035;
RA Chun H.J., Zheng L., Ahmad M., Wang J., Speirs C.K., Siegel R.M.,
RA Dale J.K., Puck J., Davis D., Hall C.G., Skoda-Smith S.,
RA Atkinson T.P., Straus S.E., Ienardo M.J.,
RT "Pleiotropic defects in lymphocyte activation caused by caspase-8
RT mutations lead to human immunodeficiency.";
RL Nature 419:395-399 (2002).
-1- FUNCTION: Most upstream protease of the activation cascade of
caspases responsible for the TNFRSF6/Fas mediated and TNFRSF1A
induced cell death. Binding to the adapter molecule FADD recruits
it to either receptor. The resulting aggregate called death-
inducing signaling complex (DISC) performs CASP8 proteolytic
activation. The active dimeric enzyme is then liberated from the
DISC and free to activate downstream apoptotic proteases.
CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
CAP5 and CAP6) are likely retained in the DISC. Cleaves and
CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
CC participate in the G2M6 apoptotic pathways. Cleaves ADPRT.
CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-I-AMC.
CC likely target for the cowpox virus CRVA death inhibitory protein.
CC Isoforms 5, 6, 7 and 8 lack the catalytic site and may interfere
CC with the pro-apoptotic activity of the complex.
-1- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 10 kDa (p10) subunit.
CC Interacts with FADD, CFLAR and PEAL5. Isoform 9 interacts at the
CC endoplasmic reticulum with a complex containing BCAP31, BAP29,
CC BCL2 and/or BCL2L1.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- ALTERNATIVE PRODUCTS:

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CC      Event=Alternative splicing; Named isoforms=9;
CC      Name=1; Synonyms=Alpha-1;
CC      IsoId=Q14790-1; Sequence=displayed;
CC      Name=2; Synonyms=Alpha-2, MCH5-beta;
CC      IsoId=Q14790-2; Sequence=VSP_000610;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:45:17 ; Search time 21 Seconds
(without alignments)
594.928 Million cell updates/sec

Title: US-10-068-564-5
1239
Perfect score: 1 MSNPRSLSEKXKMSGALA.....KARKTNPDIQSTLRKLYLQ 242
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/6C_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/6D_COMB.pep:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Length	DB	ID	Description
1	1239	100.0	242	4	US-09-187-789-5	Sequence 5, Appli
2	1065	86.0	214	4	US-09-187-789-9	Sequence 9, Appli
3	934.5	75.4	260	4	US-09-187-789-2	Sequence 2, Appli
4	934.5	75.4	260	4	US-09-139-600-2	Sequence 2, Appli
5	890	71.8	230	4	US-09-187-789-7	Sequence 7, Appli
6	293	23.6	74	4	US-09-187-789-63	Sequence 58, Appli
7	293	23.6	74	4	US-09-139-600-58	Sequence 10, Appli
8	289	23.3	421	4	US-08-983-502-10	Sequence 10, Appli
9	289	23.3	421	4	US-09-516-747-10	Sequence 10, Appli
10	289	23.3	421	5	PCT-US96-10521-10	Sequence 10, Appli
11	289	23.3	435	3	US-08-258-287B-53	Sequence 51, Appli
12	289	23.3	435	3	US-08-368-704C-51	Sequence 9, Appli
13	289	23.3	435	3	US-09-561-756-9	Sequence 9, Appli
14	289	23.3	435	4	US-09-227-721-9	Sequence 2, Appli
15	289	23.3	435	4	US-08-816-075-2	Sequence 9, Appli
16	289	23.3	435	4	US-08-724-378D-9	Sequence 9, Appli
17	289	23.3	435	4	US-09-954-697-9	Sequence 4, Appli
18	289	23.3	435	5	PCT-US94-07127A-4	Sequence 44, Appli
19	289	23.3	441	3	US-08-258-287B-44	Sequence 43, Appli
20	289	23.3	441	3	US-08-368-704C-43	Sequence 10, Appli
21	279	22.5	435	4	US-09-291-289-10	Sequence 2, Appli
22	278.5	22.1	277	2	US-08-890-542A-2	Sequence 2, Appli
23	278.5	22.1	277	3	US-08-591-605-2	Sequence 2, Appli
24	273.5	22.1	277	3	US-09-964-308-6	Sequence 6, Appli
25	273.5	22.1	277	3	US-08-462-969B-4	Sequence 6, Appli
26	273.5	22.1	277	3	US-08-964-313-6	Sequence 6, Appli
27	273.5	22.1	277	4	US-09-069-138-6	Sequence 6, Appli

28	273.5	22.1	277	4	US-09-124-934A-4	Sequence 4, Appli
29	273.5	22.1	277	4	US-08-334-251D-4	Sequence 4, Appli
30	272.5	22.0	277	4	US-09-561-756-12	Sequence 12, Appli
31	272.5	22.0	277	4	US-09-227-721-12	Sequence 12, Appli
32	272.5	22.0	277	4	US-08-983-502-30	Sequence 30, Appli
33	272.5	22.0	277	4	US-08-724-378D-5	Sequence 5, Appli
34	272.5	22.0	277	4	US-09-516-747-30	Sequence 30, Appli
35	272.5	22.0	277	4	US-09-954-697-12	Sequence 12, Appli
36	272.5	22.0	277	5	PCT-US96-10521-30	Sequence 30, Appli
37	270.5	21.8	277	4	US-09-291-289-11	Sequence 11, Appli
38	263.5	21.3	277	3	US-08-964-308-10	Sequence 10, Appli
39	263.5	21.3	277	3	US-08-964-313-10	Sequence 10, Appli
40	263.5	21.3	277	4	US-09-069-138-10	Sequence 10, Appli
41	257	20.7	503	3	US-08-258-287B-36	Sequence 36, Appli
42	257	20.7	503	3	US-08-368-704C-36	Sequence 36, Appli
43	256	20.7	303	4	US-09-561-756-24	Sequence 24, Appli
44	256	20.7	303	4	US-09-227-721-24	Sequence 24, Appli
45	256	20.7	303	4	US-08-556-627A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-187-789-5
; Sequence 5, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemti, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-5

Query Match 100.0%; Score 1239; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 3.2e-122;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSNPRSLSEKXKMSGALALILCVTKARSGSEEDIDALHMFROLRFESTMKRDPFAEQ	60
DB	1	MSNPRSLSEKXKMSGALALILCVTKARSGSEEDIDALHMFROLRFESTMKRDPFAEQ	60
QY	61	FOELEKFGQALISREDPVSCAFVVMMAHREBGFKEGDEMYKLELFEALNNKNCAL	120
DB	61	FOELEKFGQALISREDPVSCAFVVMMAHREBGFKEGDEMYKLELFEALNNKNCAL	120
QY	121	RARKXYIIOACGEORDPETVGGDEIYVWIKDSFOTIPTYTDALHVSIVGCIYAPRH	180
DB	121	RARKXYIIOACGEORDPETVGGDEIYVWIKDSFOTIPTYTDALHVSIVGCIYAPRH	180
QY	181	DQKSCFIQTLVDVFTFRKGIHLLTEVTRMAEALVQEGKARKTNPEIQSTLRKLY	240
DB	181	DQKSCFIQTLVDVFTFRKGIHLLTEVTRMAEALVQEGKARKTNPEIQSTLRKLY	240
QY	241	LQ 242	
DB	241	LQ 242	

RESULT 2
US-09-187-789-9
; Sequence 9, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:

```

; APPLICANT: Alnemri, Emed S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-9
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Query Match      86.0%; Score 1065; DB 4; Length 214;
Best Local Similarity 88.0%; Pred. No. 5.3e-10;
Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
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QY 1 MSNRSLSLEEKYDMSGALALILCVTKARSGSEEDLDALBHMFRQLRPESTMKRDPTAAEQ 60
D 1 MSNRSLSLEEKYDMSGALALILCVTKARSGSE-----34
QY 61 FOEIEKFOQAIDSRDPVSCAFVYLMAGREGFLKGDGEMVYLENLFEALNNKNCQAL 120
D 35 --EIEKFOQAIDSRDPVSCAFVYLMAGREGFLKGDGEMVYLENLFEALNNKNCQAL 92
QY 121 RAKPKVYIIQACRGEGQDPGETVGDEIVAWYIKDSPOTIPYTDALHVSIVSEGYYARRH 180
D 93 RAKPKVYIIQACRGEGQDPGETVGDEIVAWYIKDSPOTIPYTDALHVSIVSEGYYARRH 152
QY 181 DQKSGSCITQTLVDVFTFKRKHILLELTVTRMAAEELVQEGARKATNPEIQSTLRKELY 240
D 153 DQKSGSCITQTLVDVFTFKRKHILLELTVTRMAAEELVQEGARKATNPEIQSTLRKELY 212
QY 241 LQ 242
D 213 LQ 214

RESULT 3
US-09-187-789-2
; Sequence 2, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-2
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Query Match      75.4%; Score 934.5; DB 4; Length 260;
Best Local Similarity 70.9%; Pred. No. 3.6e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
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```

QY 1 MSNRSLSLEEKYDMSGALALILCVTKARSGSEEDLDALBHMFRQLRPESTMKRDPTAAEQ 60
D 8 MSDDPQLQBERYDMSGARLALILCVTKARSGSEVDMEALBMRFLKPESTMKRDPTAAEQ 67
QY 61 FOEIEKFOQAIDSRDPVSCAFVYLMAGREGFLKGDGEMVYLENLFEALNNKNCQAL 120
D 68 FLEIEDEFOQTIDMEBEPVSCAFVYLMAGREGFLKGDGEMVYLENLFEALNNKNCQAL 127
QY 121 RAKPKVYIIQACRGEGQDPG-----ETVGGDEIVAWYIKDSPOTIPYTDALHVS 168
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D 128 RKPCKVYIIQACRGHRDPGEBELRGNEELGDEBELGDE-VAVLKNNGQSIPTTYDTLHI 186
QY 169 YSTVGGYIAYRRDQSGSCITQTLVDVFTFKRKHILLELTVTRMAAEELVQEGARKATN 228
D 187 YSTVGGYIAYRRDQSGSCITQTLVDVFTFKRKHILLELTVTRMAAEELVQEGARKATN 246
QY 229 PEIQSTLRKRLYLQ 242
D 247 PEVQSTLRKRLYLQ 260
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RESULT 4
US-09-139-600-2
; Sequence 2, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-2
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Query Match      75.4%; Score 934.5; DB 4; Length 260;
Best Local Similarity 70.9%; Pred. No. 3.6e-90;
Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;
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QY 1 MSNRSLSLEEKYDMSGALALILCVTKARSGSEEDLDALBHMFRQLRPESTMKRDPTAAEQ 60
D 8 MSDDPQLQBERYDMSGARLALILCVTKARSGSEVDMEALBMRFLKPESTMKRDPTAAEQ 67
QY 61 FOEIEKFOQAIDSRDPVSCAFVYLMAGREGFLKGDGEMVYLENLFEALNNKNCQAL 120
D 68 FLEIEDEFOQTIDMEBEPVSCAFVYLMAGREGFLKGDGEMVYLENLFEALNNKNCQAL 127
QY 121 RAKPKVYIIQACRGHRDPG-----ETVGGDEIVAWYIKDSPOTIPYTDALHVS 168
D 128 RKPCKVYIIQACRGHRDPGEBELRGNEELGDEBELGDE-VAVLKNNGQSIPTTYDTLHI 186
QY 169 YSTVGGYIAYRRDQSGSCITQTLVDVFTFKRKHILLELTVTRMAAEELVQEGARKATN 228
D 187 YSTVGGYIAYRRDQSGSCITQTLVDVFTFKRKHILLELTVTRMAAEELVQEGARKATN 246
QY 229 PEIQSTLRKRLYLQ 242
D 247 PEVQSTLRKRLYLQ 260
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RESULT 5
US-09-187-789-7
; Sequence 7, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 230
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TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-7

Query Match 71.8%; Score 890; DB 4; Length 230;
Best Local Similarity 99.4%; Pred. No. 1.5e-85;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNRSLEEEKYDMSGALALILCVTKARSGSEEDLDLEHMFQRLPFESTMKRDPTAEQ 60
DB 1 MSNRSLEEEKYDMSGALALILCVTKARSGSEEDLDLEHMFQRLPFESTMKRDPTAEQ 60
QY 61 FOEELKFOQAIDSREDVSCAFVILMAHREGFLKGDGEMVKLENLFEALNNKQCAL 120
DB 61 FOEELKFOQAIDSREDVSCAFVILMAHREGFLKGDGEMVKLENLFEALNNKQCAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGDEIVMTIKDSPQITPTTDAIHVSTVEG 174
DB 121 RAKPKVYIIQACRGQRDPGETVGDEIVMTIKDSPQITPTTDAIHVSTVEG 174

RESULT 6
US-09-187-789-63

Sequence 63, Application US/09187789

Patent No. 6340740

GENERAL INFORMATION:

APPLICANT: Alnemri, Emdad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: 480140.434C1

CURRENT APPLICATION NUMBER: US/09/187,789

CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 63

LENGTH: 74

TYPE: PRT

ORGANISM: Mus musculus

US-09-187-789-63

Query Match 23.6%; Score 293; DB 4; Length 74;
Best Local Similarity 77.8%; Pred. No. 1.6e-23;
Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 28 ARGSEEDLDLEHMFQRLPFESTMKRDPTAEQFOEELKFOQAIDSREDVSCAFVILM 87
DB 1 ARGSEEDLDLEHMFQRLPFESTMKRDPTAEQFOEELKFOQAIDSREDVSCAFVILM 87

QY 88 AHREGFLKGED 99
DB 61 AHREGFLKGED 72

RESULT 7
US-09-139-600-58

Sequence 58, Application US/09139600

Patent No. 6432628

GENERAL INFORMATION:

APPLICANT: Alnemri, Emdad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING

TITLE OF INVENTION: AND METHOD OF USE

FILE REFERENCE: 480140.434

CURRENT APPLICATION NUMBER: US/09/139,600

CURRENT FILING DATE: 1998-08-25

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 58

LENGTH: 74

TYPE: PRT

ORGANISM: Mus musculus

US-09-139-600-58

Query Match 23.6%; Score 293; DB 4; Length 74;
Best Local Similarity 77.8%; Pred. No. 1.6e-23;
Matches 56; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 28 ARGSEEDLDLEHMFQRLPFESTMKRDPTAEQFOEELKFOQAIDSREDVSCAFVILM 87
DB 1 ARGSEEDLDLEHMFQRLPFESTMKRDPTAEQFOEELKFOQAIDSREDVSCAFVILM 87

QY 88 AHREGFLKGED 99
DB 61 AHREGFLKGED 72

RESULT 8
US-08-983-502-10

Sequence 10, Application US/08983502

Patent No. 6399327

GENERAL INFORMATION:

APPLICANT: David WALLACH

APPLICANT: Mark P. BOLDIN

APPLICANT: Tanya M. GONCHAROV

TITLE OF INVENTION: YUZY V. GOLTSSEV

TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSER: Broadway and Neimark

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/983,502

FILING DATE: 16-JAN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10521

FILING DATE: 14-JUN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114,615

FILING DATE: 16-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 114,986

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 115,319

FILING DATE: 14-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 116,588

FILING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: IL 117,932

FILING DATE: 16-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Broadway, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: WALLACH=19

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 421 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein


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QY      29  EGGSEEDIDALEHMRQRLFEESTMKRDPRAEFOEIELEKFOOAI8RDERPVSCAFVLMA  88
Dh      188  RSGGVNDSTLVTFLKLGVDVHVLCDQTAQEMQKQLQFPAQ-LPRHRTYDSC-YALLLS  245
QY      89  HGRGEFLGEGDEMWKLENTPEALNNKNCQALRAKPKYVLIQA9CRGEQD9PG-----  140
Dh      246  HGVEBAIVGVDQKLLQLEVFQLEFDPNACPSLQNKREKMFPIQA9CRGDEDTEDRGDQDQXN  305
QY      141  -----ETVGGDEIVMVIKDSFQIPIFYTALNHYSVEGIAARHQQSGSCFQTV  192
Dh      306  HAGSDGCEESDQKGE-----KLPRKRLPPRSDITCGYALCLKGTAAMENITKGSWYTEALA  360
QY      193  DVETFR--KGHILELLEVTTRMAAEALVQEGCARKTN-----PEI0STLKRRIYL  241
Dh      361  QVFSERACMCHVADMLVKYNALLIKD---REGVAPQTEPHRCCKEMSPSYGTLCRHLYL  414

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1      RESULT 11
2      US-08-258-287B-53
3      / Sequence 53, Application US/08258287B
4      / Patent No. 6083735
5      / GENERAL INFORMATION:
6      / APPLICANT: Yuan, Junying
7      / APPLICANT: Mura, Masayuki
8      / TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
9      / NUMBER OF SEQUENCES: 85
10     / CORRESPONDENCE ADDRESS:
11     / ADDRESS: Sterne, Kessler, Goldstein & Fox
12     / STREET: 1100 New York Avenue, Suite 600
13     / CITY: Washington
14     / STATE: D.C.
15     / COUNTRY: USA
16     / ZIP: 20005
17     / COMPUTER READABLE FORM:
18     / MEDIUM TYPE: Floppy disk
19     / COMPUTER: IBM PC compatible
20     / OPERATING SYSTEM: PC-DOS/MS-DOS
21     / SOFTWARE: PatentIn Release #1.0, Version #1.25
22     / CURRENT APPLICATION DATA:
23     / APPLICATION NUMBER: US/08/258,287B
24     / FILING DATE: 10-JUN-1994
25     / CLASSIFICATION: 435
26     / PRIOR APPLICATION DATA:
27     / APPLICATION NUMBER: US 08/080,850
28     / FILING DATE: 24-JUN-1993
29     / ATTORNEY/AGENT INFORMATION:
30     / NAME: Bugalsky, Lawrence B.
31     / REGISTRATION NUMBER: 35,086
32     / REFERENCE/DOCKET NUMBER: 0609.3920001
33     / TELECOMMUNICATION INFORMATION:
34     / TELEPHONE: (1202) 371-2600
35     / TELEFAX: (202) 371-2540
36     / TELEX: 248636 SSK
37     / INFORMATION FOR SEQ ID NO: 53:
38     / SEQUENCE CHARACTERISTICS:
39     / LENGTH: 435 amino acids
40     / TYPE: amino acid
41     / TOPOLOGY: linear
42     / MOLECULE TYPE: protein
43     /
44     / US-08-258-287B-53

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Query Match	23.3%	Score 289;	DB 3;	Length 435;
Best Local Similarity	31.1%	Pred. No. 5.4e-22;		
Matches 74;	Conservative 51;	Mismatches 77;	Indels 36;	Gaps 7.

Qy 29 REGSEEDIDALHMFEOLEFESTMKDDPAAEOQOELETERKOQALIBREBVSAAVWMA 38

Db 202 RSGGVDSHTVTLFLKLLGYDVHVLCDQJAAEMQEXKUNPAO-LPAHRVDS-C-1VALTS 259

Qy 89 HGRBGLKGEDESMVKTENLPEALANKNCQALPAKRVYITLQCRBQBPBG----- 140

Db 260 HVEVEAIVGDDKTLQLOEVPQLDENANCSTLONKREMPFTQCRGGEJDRGVDDQDQGN 31,9

```

QY -----ETVGGSEIVAVINDSPQTIIPTDYLALHYSTVEGVYIAVRHDKQSCSEFQIVL 192
Db 320 HAGSPGCEESQAGK-----KLPRKRLPTPSMIGCYACIKTAAAMRNKRSQSWYTEALA 374
QY 193 DVFFKKR--KGIITLLEITVTRRMAEVLVEQKARKTN-----PEIQTIRKRLYL 241
Db 375 QVFSRRACDMIVADMLVKNMLIK-----REUYAGTEPHRCCKEMSEYGCSTCRHLYL 428

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1      RESULT 12
2      US-08-368-704C-51
3      / Sequence 51. Application US/08368704C
4      / Patent No. 6087160
5      / GENERAL INFORMATION:
6      / APPLICANT: Yuan, Junying
7      / APPLICANT: Miura, Masayuki
8      / TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
9      / NUMBER OF SEQUENCES: 95
10     / CORRESPONDENCE ADDRESS:
11     / ADDRESSEE: Sterne, Kessler, Goldstein & Fox
12     / STREET: 1100 New York Avenue, Suite 600
13     / CITY: Washington
14     / STATE: D.C.
15     / COUNTRY: USA
16     / ZIP: 20005
17     / COMPUTER READABLE FORM:
18     / MEDIUM TYPE: Floppy disk
19     / COMPUTER: IBM PC compatible
20     / OPERATING SYSTEM: PC-DOS/MS-DOS
21     / SOFTWARE: Patentln Release #1.0, Version #1.25
22     / CURRENT APPLICATION DATA:
23     / APPLICATION NUMBER: US/08/368,704C
24     / FILING DATE: 4-JAN-1995
25     / CLASSIFICATION: 435
26     / PRIOR APPLICATION DATA:
27     / APPLICATION NUMBER: US 08/258,287
28     / FILING DATE: 10-JUN-1994
29     / CLASSIFICATION: 435
30     / PRIOR APPLICATION DATA:
31     / APPLICATION NUMBER: US 08/080,850
32     / FILING DATE: 24-JUN-1993
33     / ATTORNEY/AGENT INFORMATION:
34     / NAME: Bugalsky, Lawrence B.
35     / REGISTRATION NUMBER: 35,086
36     / REFERENCE/DOCKET NUMBER: 0609.3920002
37     / TELECOMMUNICATION INFORMATION:
38     / TELEPHONE: (202) 371-2600
39     / TELEFAX: (202) 371-2540
40     / TELEX: 248636 BSK
41     / INFORMATION FOR SEQ ID NO: 51:
42     / SEQUENCE CHARACTERISTICS:
43     / LENGTH: 435 amino acids
44     / TYPE: amino acid
45     / TOPOLOGY: linear
46     / MOLECULE TYPE: protein
47     /
48     / US-08-368-704C-51

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Query Match	23.3%;	Score 289;	DB 3;	Length 435;
Best Local Similarity	31.1%;	Pred. No. 5.4e-22;		
Matches	74;	Conservative	51;	Mismatches 77;
				Indels 36;
				Gaps 77;

QY 29 REGSEEDJADALENHMRÖLREBS IMKRDPIAEQFUEBLEFQVALLURSEFVJATVLLA
Db 202 RSGGVDSHTVTLFKLGYDVHVACDQTAQMOEKLQNEAQ-LPHRVYDSC-VALLS 259
QY 89 HGRSEFGLGEDEMWKLENFLEALNNKCOALRAKPKVYIQA3CEGEORDPG-----140
Db 260 HGVBESALITGVQSKLLQLEQVFQFLPDNANCPSPONKEKMFETIOACRDEDETRGVDOODGKN 319
QY 141 -----FYGGSEDIWVWIKDSQCTIPITYTALHYSTVEGIIA3RHQKGGCITQYV 192
Db 320 HNGSGCEESDAGKE-----KLKPKRILPIRSMITCYAALCKGTAAANRNTRKSGSWYTEALA 374

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:44:06 ; Search time 17.5 Seconds
(without alignments)
1330.191 Million cell updates/sec

Title: US-10-068-564-5

Perfect score: 1239

Sequence: 1 MSNPRSLBEKXKMSGALAL.....KARKTNPEIQSTLRRLRYLQ 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	99.6	242	2	JC7517
2	293	93.6	452	2	JC6507
3	289	23.3	435	2	A54821
4	282.5	22.8	277	2	JC5410
5	280.5	22.6	277	2	S64710
6	272.5	22.0	277	2	A55315
7	264.5	21.3	454	2	JC7123
8	248.5	20.1	503	2	A49429
9	246.5	19.9	212	2	I67437
10	239.5	19.3	416	2	G02655
11	230	18.6	495	2	T20038
12	226	18.2	311	2	B56084
13	226	18.2	383	2	A56084
14	226	18.2	404	2	A42677
15	225	18.2	418	2	B57511
16	217.5	17.6	402	2	A46495
17	213.5	17.2	182	2	I67436
18	210.5	17.0	826	2	T43638
19	207	16.7	263	2	C56084
20	205.5	16.6	377	2	A57511
21	197	15.9	312	2	B54821
22	189	15.3	536	2	T43633
23	185	14.9	488	2	T13385
24	174.5	14.1	642	2	T27021
25	159.5	12.9	136	2	I53300
26	103.5	8.4	1313	2	A48467
27	98	7.9	1957	2	A45627
28	97.5	7.8	139	2	T43642
29	97	7.8	1051	2	T18302

30	95.5	7.7	1190	2	E84193
31	95.5	7.7	2104	2	T38774
32	95	7.7	761	2	B82205
33	91	7.3	394	2	T26968
34	91	7.3	510	2	S42626
35	90.5	7.3	520	2	F70350
36	89.5	7.2	467	2	D95253
37	89.5	7.2	482	2	B98118
38	89.5	7.2	1225	2	A56514
39	89	7.2	352	2	T43328
40	88.5	7.1	149	2	T43637
41	88.5	7.1	661	2	B97733
42	88.5	7.1	858	1	I4RTNC
43	88.5	7.1	1203	2	B55094
44	88.5	7.1	2954	2	T14156
45	88	7.1	505	2	S39520

ALIGNMENTS

chromosome segrega
myosin-3 heavy cha
chemotaxis protein
hypothetical prote
ER-golgi intermed
recombination prot
L-fuculose kinase
rhamnulokinase (EC
chromokinesin - ch
probable flagellar
caspase protein 1C
excinuclease ABC s
neural cell adhesi
chromosomal protei
kinesin-related pr
H+-transporting tw

RESULT 1
JC7517
caspase-14/a - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C/Accession: JC7517
R/Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.
Biochem. Biophys. Res. Commun. 277, 655-659, 2000
A/Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyt
A/Reference number: JC7517; PMID:20517231; PMID:11062009
A/Contents: Epidermal keratinocytes
A/Accession: JC7517
A/Molecule type: mRNA
A/Residues: 1-242 <ECK>
A/Cross-references: GB:AF097874
C/Comment: This enzyme accumulates during keratinocyte differentiation and is activate
C/Genetics:
A:Gene: casp-14/a
A:Map position: 19p13.1
A:Introns: 9/3; 59/3; 135/1; 174/1; 208/3
C/Keywords: differentiation

Query Match 99.6%; Score 1234; DB 2; Length 242;
Best Local Similarity 99.6%; Pred. No. 1.2e-88;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MSNPRSLBEKXKMSGALALILCVTKARSGSEDDIDALEHMPROLFEESTMRDPTAQ 60
DB	1	MSNPRSLBEKXKMSGARLALILCVTKARSGSEDDIDALEHMPROLFEESTMRDPTAQ 60
QY	61	FOELEKFOQALDSREDPVSCAFVIMAHGRSGFLKGEDEGVYKLENIFFALNNKCOAL 120
DB	61	FOELEKFOQALDSREDPVSCAFVIMAHGRSGFLKGEDEGVYKLENIFFALNNKCOAL 120
QY	121	RAPKXYIIIOACGEQDPETVSGDEIYVNIWIDSPOTITPYDIALHVSTVSGIYVRH 180
DB	121	RAPKXYIIIOACGEQDPETVSGDEIYVNIWIDSPOTITPYDIALHVSTVSGIYVRH 180
QY	181	DQGSCTIOTLVVFTFKRGHIELLFEVRRMAEALVOEGARKTNPEIQSTLRRLY 240
DB	181	DQGSCTIOTLVVFTFKRGHIELLFEVRRMAEALVOEGARKTNPEIQSTLRRLY 240
QY	241	IQ 242
DB	241	IQ 242

RESULT 2
JC6507
caspase-2 - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C/Accession: J06507
 R/Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
 Gene 202, 127-132, 1997
 A/Title: Cloning and expression of the cDNA encoding rat caspase-2.
 A/Reference number: J06507; MUID:96087427; PMID:9427555
 A/Accession: J06507
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-452 <SAR>
 A/Cross-references: GB:U77933; NID:g2769705; PIND:AMB96379.1; PID:g2769706

Query Match 23.6%; Score 293; DB 2; Length 452;
 Best Local Similarity 31.5%; Pred. No. 3e-15;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY REGSEEDLDALHMFROLPFESTMKRDPPTAQOELEKFOQALDSREDPVSQAFVYMA 88
 Db RSGGDVHTTLVTLFKLGINVHVLVDQAEWQEKLFQNFQO-LPAHRTVDSG-IVALIS 276
 QY HGRBGLFKGEDGEMVKLENLFEALNNKNCQALRAKPKYIIQAQCRGEBRDPG----- 140
 Db HGVGGIYGVGDKLQOEVRFLPDNANCPSLQNKPMFIIQAQCRGDETRGVDDQDGN 336
 QY 141 -----ETVGGDEIWMVTKDSPTIPTYTDALHYSTVEGYIAYRHQKSGCFIQTLY 192
 Db 337 HAOSPGCESDADAGEBEIMKMR-----LPTSDMICGYACLKGNAMENTKRGSWYIALT 391
 QY 193 DVEFTKR--KGHILELLETVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241
 Db 392 QVFSERACDMHADMVKVNALIKD---REGIAPGTEPHRCKEMSEYCSLTCQQLYL 445

RESULT 3

A54821
 apoptosis regulator ICH-1, stimulatory form L - human

C/Species: Homo sapiens (man)
 C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C/Accession: A54821
 R/Wang, L.; Mura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
 Cell 78, 739-750, 1994

A/Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
 A/Reference number: A54821; MUID:94373811; PMID:8087842
 A/Accession: A54821
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-435 <MAN>

A/Cross-references: GB:U13021; NID:9537291; PID:9537292
 C/Keywords: alternative splicing; apoptosis

Query Match 23.3%; Score 289; DB 2; Length 435;
 Best Local Similarity 31.1%; Pred. No. 5.9e-15;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEEDLDALHMFROLPFESTMKRDPPTAQOELEKFOQALDSREDPVSQAFVYMA 88
 Db 202 RSGGDVHTTLVTLFKLGINVHVLVDQAEWQEKLFQNFQO-LPAHRTVDSG-IVALIS 259
 QY HGRBGLFKGEDGEMVKLENLFEALNNKNCQALRAKPKYIIQAQCRGEBRDPG----- 140
 Db 260 HGVGGIYGVGDKLQOEVRFLPDNANCPSLQNKPMFIIQAQCRGDETRGVDDQDGN 319
 QY 141 -----ETVGGDEIWMVTKDSPTIPTYTDALHYSTVEGYIAYRHQKSGCFIQTLY 192
 Db 320 HNSPGCESDADAGE-----KLPMKMLPTPSDMI CGYACLKGNAMENTKRGSWYIALA 374
 QY 193 DVEFTKR--KGHILELLETVTRMAEALVQEGKARKTN-----PEIQSTLRKRLYL 241
 Db 375 QVFSERACDMHADMVKVNALIKD---REGIAPGTEPHRCKEMSEYCSLTCRHLYL 428

RESULT 4
 J05410
 CPP32 protein - mouse

C/Species: Mus musculus (house mouse)
 C/Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 17-Mar-1999
 C/Accession: J05410
 R/Mukasa, T.; Uraae, K.; Momoi, M.Y.; Kimura, I.; Momoi, T.
 Biochem. Biophys. Res. Commun. 231, 770-774, 1997
 A/Title: Specific expression of CPP32 in sensory neurons of mouse embryos and activatio
 A/Reference number: J05410; MUID:97224429; PMID:9070890
 A/Accession: J05410
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-277 <MDK>
 A/Cross-references: DDBJ:D86352
 A/Experimental source: embryo
 C/Comment: This protein is involved in the apoptosis of dorsal root ganglia neurons.

Query Match 22.8%; Score 282.5; DB 2; Length 277;
 Best Local Similarity 32.4%; Pred. No. 1.1e-14;
 Matches 81; Conservative 38; Mismatches 104; Indels 27; Gaps 8;

QY 9 EKYDMSGALALILCVT-----KAREGEEDLDALHMFROLPFESTMKRDPPTA 58
 Db 34 DSSYKMDYPMGCIITITNNKFNHKTGMSRSRGTDVAANIRETFMGLKYEVRKNLDR 93
 QY EOPQOELEKFOQALDSREDPVSQAFVYMAHGRBGLFKGEDGEMVKLENLFEALNNKNCQ 118
 Db 94 EETMELMDSVSKEDHSKRSFVC--VLIHSGEGVIFGNGP-VDLKILTSFPGDYCR 149
 QY 119 ALRAKPKYIIQAQCRGEBRDPG-ETVGGDEIWMVTKDSPTIPTYTDALHYSTVEGYIA 177
 Db 150 SLTKGKPLFIQAQCRGTELDGCIETDSGTDEEMAC-----QKIPVADFLVAYSTAPYIS 205
 QY 178 YRHQKSGCFIQTLYVDVFTYRKGHILE--LILVTRMA-----EALVQEGKARKTNPE 230
 Db 206 WRNSKQSGWFIQSLCSML-KLYAHKLEFMHILTRVNRKATERSFSLDSTFAKKQIPC 264
 QY 231 IOSTLRKRLYL 240
 Db 265 IVSMLTRKLY 274

RESULT 5

S64710
 cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster

C/Species: Cricetulus griseus (Chinese hamster)
 C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
 C/Accession: S64710; S72395
 R/Wang, X.; Zelenski, N.G.; Yang, J.; Sakai, J.; Brown, M.S.; Goldstein, J.L.
 EMBO J. 15, 1012-1020, 1996

A/Title: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 during
 A/Reference number: S64710; MUID:96183185; PMID:8605870
 A/Accession: S64710
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-277 <MAN>

A/Cross-references: EMBL:U27463
 R/Wang, X.
 submitted to the EMBL Data Library, May 1995
 A/Reference number: S72395
 A/Accession: S72395

A/Molecule type: mRNA
 A/Residues: 1-79, 'A', 81-146, 'Y', 148-277 <MAN>
 A/Cross-references: EMBL:U27463; NID:g1244443; PIND:AA01511.1; PID:g1244444
 C/Keywords: apoptosis; cysteine proteinase; hydrolase

Query Match 22.6%; Score 280.5; DB 2; Length 277;
 Best Local Similarity 35.9%; Pred. No. 1.6e-14;
 Matches 79; Conservative 31; Mismatches 93; Indels 17; Gaps 7;

QY 29 REGSEEDLDALHMFROLPFESTMKRDPPTAQOELEKFOQALDSREDPVSQAFVYMA 88
 Db 64 RSGTDVDAKARETFMNLKYEVNRKNNDLREIIVEIMKNASKEDHSKRSFVC--VLIIS 120
 QY 89 HGRBGLFKGEDGEMVKLENLFEALNNKNCQALRAKPKYIIQAQCRGEBRDPG-ETVGGDE 147

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Db      121 HGDEGVIPGTGCP-IDLKKLTSTYFGDRBCRSLLIGPKFLFIQACGTELDGIEFDSCGTE 179
QY      148 IWMVTKDSPTPTPTDMLHYVSTEGYIAYRHDKGSCFIQTVLVDVETKRGHILE--- 204
Db      180 DDMTC---QKIPVADDFIYAVSTAPGIYSWNPDPDGSFISLOSLCML-KIYAHLEPMH 234
QY      205 LITEVTRMA---EAEIVQEGKARKTNEIOLSTLRKRLY 240
Db      235 ILTRVNRKVAETEFESFSLDSTFHAKKQIFCIYSMLTKELY 274

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RESULT 6
cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human
A55315

N.Alternate names: cysteine proteinase CPP32
C.Species: Homo sapiens (man)
C.Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
C.Accession: A55315; S58899; I39005
R.Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A.Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans
A.Reference number: A55315; MUID:95074038; PMID:7983002
A.Accession: A55315
A>Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-277 <PER>
A.Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666
R.Nicholson, D.M.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant, M.; Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A.Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian
A.Reference number: S58899; MUID:95319529; PMID:7596430
A.Accession: S58899
A.Molecule type: protein
A.Molecule type: protein
A.Residues: 29-46; 116-189, 'E', 191-193 <NIC>
R.Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poirier, Cell 81, 801-809, 1995
A.Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease
A.Reference number: A56924; MUID:95292347; PMID:7774019
A.Accession: I39005
A>Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-189, 'E', 191-277 <RGS>
A.Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569
C.Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 22.0%; Score 272.5; DB 2; Length 277;
Best Local Similarity 31.9%; Pred. No. 6.5e-14;
Matches 80; Conservative 39; Mismatches 103; Indels 29; Gaps 9;

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QY      9 EEKYDMSGALALILCVTK-----AREGSEEDLALHEMFQRLFEESTMKRDP7A 58
Db      34 DNSYKMDYPRMGCTIINNKNFHKSTMTSRSGTDVDAALREFRNLKTEVRNKKDLTR 93
QY      59 EGFQSELEKEQQAIDSRDPVSCAFVVLMAHGRGFLKGDG--EWVKLENLEALNNKN 116
Db      94 EELVELMRDYSKHEHSRRSPVC---VLSHGEGLIFGNGPVDLKKINFF---RGDR 147
QY      117 QQALRAKPYVITIQACGEQDPG-ETVVGDEIYMWIKDSPTPTPTDMLHYSTYEGY 175
Db      148 CRSLTGKPKLFIQACRGTELDGIEFDSDGVDMMAC---HKLPVADDFIYAVSTAPGY 203
QY      176 IAYRHDKGSCFIQTVLVDVETK--RKGHILELLETVTRMA-EAEIVQ---EGARKTNP 229
Db      204 YSMWNSKDGSWFISLCAMLKQYADKLEFMHILTRVNRKVAETEFESFPAITFAKKQIF 263
QY      230 EIOSTLRKRLY 240
Db      264 CIYSMLTKELY 274

```

RESULT 7

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JC7123
caspase-9 long chain - mouse
C.Species: Mus musculus (house mouse)
C.Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C.Accession: JC7123
R.Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A.Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9
A.Reference number: JC7123; MUID:20001956; PMID:10529400
A.Accession: JC7123
A>Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-454 <FUJ>
A.Cross-references: DDBJ:AB019600; NID:96440941; PID:96440942

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Query Match 21.3%; Score 264.5; DB 2; Length 454;
Best Local Similarity 30.6%; Pred. No. 4.9e-13;
Matches 76; Conservative 36; Mismatches 89; Indels 47; Gaps 7;

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QY      29 REGSEEDLALHEMFQRLFEESTMKRDP7AEG---FQSELEKFOQAIDSRDPVSCAFV 84
Db      218 RFGSNIDRDKLEHRRFRMLRFVVEVKNDDLAKKMTALMEMAHNRHPLD-----CFVY 270
QY      85 VIMAHGRE-----GFLKGEDENVYKLENLEFALNNKNQQAALRAKPYVITIQACGEOR 137
Db      271 VILSHCCQASHIQFGAVVGTGDCSVSTIKYININSGSCPSLGGKPKLFIQACGGEQK 330
QY      138 D-----FETVGGDEIYMWIK-----DSQITIPYTDMLHYSTYEGYI 176
Db      331 DGFVEVACTSSQGRITLDSSEPDATPFQGPSPDLDLAVSSLFPSPDILVSYTFPGFV 390
QY      177 AYRHDKGSCFIQTVLVDVETK--RKGHILELLETVTRMAEAEIVQEGKARKTNP1QST 234
Db      391 SWRDKKSGSWYLETLDGILFQWARSBDLSLILRV-----ANAVSEKGTQKIPGCFNF 444
QY      235 LKRLIYLO 242
Db      445 LKKKLPFK 452

```

RESULT 8

A49429
interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C.Accession: A49429; T37312
R.Yuan, J.; Shaham, S.; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
Cell 75, 641-652, 1993
A.Title: The C. elegans cell death gene ced-3 encodes a protein similar to mammalian
A.Reference number: A49429; MUID:94061982; PMID:8242740
A.Accession: A49429
A>Status: preliminary
A.Molecule type: DNA
A.Residues: 1-503 <YUA>

A.Cross-references: GB:U29052; NID:96503232; PIDN:AAA27982.2; PID:96503233
A.Note: sequence extracted from NCBI backbone (NCBI:U139825, NCBI:P139826)
A.Accession: T37312
A>Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-417, 'R', 419-503 <YU2>
A.Cross-references: EMBL:U29052; PIDN:AAA27982.1
C.Genetics:
A.Gene: ced-3
A.Introns: 45/3; 94/2; 179/1; 289/3; 361/1; 403/3; 483/3

Query Match 20.1%; Score 248.5; DB 2; Length 503;
Best Local Similarity 27.9%; Pred. No. 9.8e-12;
Matches 68; Conservative 42; Mismatches 93; Indels 41; Gaps 6;

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QY      29 REGSEEDLALHEMFQRLFEESTMKRDP7AEGFQSELEKFOQAIDSRDPVSCAFVIMA 88
Db      259 RNGTKADKXNLTNLFRCMGYTVICKDNLTRGMULTIRDFAK---HSHSDSAIIVLIS 314

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QY 89 HGRGEGFLKGEDEGMVKNLEFALNNKNCQALRAKPKYIIIOACRGQRDPGETV----- 143
 Db 315 HGEENVIIIGVDIPISTHEIYDLNNAANAPRLANKKIVFOACGGERDNGFPLDSVD 374
 QY 144 -----GGEIYVWITDSP-----OTIFTYDALHYSTVEGYTAJR 179
 Db 375 GVPAPFLRRGMWN-----RDGPLEFNLGCVRPQVOQWMEKPSQADILLIAYATTAQYVSWR 429
 QY 180 HDQKSGCFIQTLDVFT--KRKGHILELLETVTRRMAAEIYVQSG-KARKTNPEIQTSLR 236
 Db 430 NSAGSMFIOAVCEVFSHTAKMDVVELLITVNNKKVACGFTSGSNTLKQMPMTSRL 489
 QY 237 KRLTY 240
 Db 490 KKFY 493

RESULT 9

167437
 cysteine proteinase (EC 3.4.22.-) P32 - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C/Accession: I67437
 R/Name: J.A.; Kugu, K.; Tshovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfield, A.N.; Tili
 Endocrinology 136, 5042-5053, 1995
 A/Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
 nuloa cells of the ovarian follicle.
 A/Reference number: 153300; MUID:96042509; PMID:7588240
 A/Accession: I67437
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-212 <RES>
 A/Cross-references: EMBL:U34685; NID:g1004370; PIDN:AAC52261.1; PID:g1004371
 C/Keywords: cysteine proteinase; hydrolase

Query Match 19.9%; Score 246.5; DB 2; Length 212;
 Best Local Similarity 31.5%; Pred. No. 5e-12;
 Matches 69; Conservative 34; Mismatches 89; Indels 27; Gaps 8;

QY 9 EEKYDMSGALALILCVT-----KAREGSEEDLALHEMFQOLRFESTMKDPTA 58
 Db 5 DSSYKMDPYEMGCLTIINKNFKSTGMSKANGIDVDANLRETFALKTEVANKKDLTR 64
 QY 59 EGFQEELEKFOQALIDREDPVSCAFVVLMAHGREGLKGEHGMVLENIFFALNNKNCQ 118
 Db 65 EEIMEIMDSVSKDHSKRSSFVC---VILSHGDEGVIFGNGP-VDLKLTLSFFRDYCR 120
 QY 119 ALRAKRVITIOCRGEQDPG-ETVGG--DEIVMWIKDSPQTIPTYTALHYSTVEGY 175
 Db 121 SLTGKPKLFIQACRGTEIDSGIETDSGADDDVAC-----QKKPYEADFLVYSSAPGY 174
 QY 176 IAYRHQKSGCFIQTLDVFTKKRGHILE--LLETVTR 211
 Db 175 YSWRNSRGSGSWFIQSLC-AMLKIVAKILFPMHILITRYNR 212

RESULT 10

G02635
 ICR-LAP6 - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
 C/Accession: G02635
 R/Name: H.; Orth, K.; Chinaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
 submitted to the EMBL Data Library, April 1996
 A/Reference number: H01513
 A/Accession: G02635
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-416 <DUA>
 A/Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027

Query Match 19.3%; Score 239.5; DB 2; Length 416;
 Best Local Similarity 28.7%; Pred. No. 3.9e-11;

Matches 72; Conservative 46; Mismatches 84; Indels 49; Gaps 9;
 QY 27 KAREGSEEDLALHEMFQOLRFESTMKADPAEFOEELKEFOQALIDRED--PVSCAFV 84
 Db 178 RRTGNSINDCKELRRRSLSHFVWVKGDLTAKKVVALLLEL-----ARQHGALDCCVV 232
 QY 65 VLMAHGNE-----GFLKGEDEGMVKNLEFALNNKNCQALRAKPKYIIIOACRGQR 137
 Db 233 VILSHGQASHLOPPGAVYGTGCGPVSVEKIVNFNGTSCPSLGGKPLFIQACGGEQK 292
 QY 138 DPG-----ETVGG-----DEIVMWIKDSPQTIPTYTALHYST 171
 Db 293 DHGEFVASTPDESPGNSNPPDATPPOEGLRTPDOL-----DAISSLPSTDIFFVAST 347
 QY 172 VEGTAYRHQKSGCFIQTLDVFTKKRGHILELLETVTRRMAAEIYVQSGKARKTPEI 231
 Db 348 FPGFVSWRDPKSGSGWYETLIDIF-EQWAF-SEDLQSLLRVANAIVSK--GIYKQMGCC 403
 QY 232 QSTLRKRLTYQ 242
 Db 404 FNFLRKXLFK 414

RESULT 11

T20038
 hypothetical protein C48D1.2 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C/Accession: T20038
 R/Burton, J.
 submitted to the EMBL Data Library, October 1996

A/Reference number: Z19214
 A/Accession: T20038
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-495 <WIL>
 A/Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2
 A/Experimental source: clone C48D1
 A/Genes: CESP:C48D1.2
 A/Map position: 4
 A/Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 18.6%; Score 230; DB 2; Length 495;
 Best Local Similarity 27.6%; Pred. No. 2.6e-10;
 Matches 60; Conservative 39; Mismatches 78; Indels 40; Gaps 5;

QY 29 REGSEEDLALHEMFQOLRFESTMKDPTAEQFQEBLEKFOQALIDREDPVSCAFVILMA 88
 Db 258 RNGTAKDXNLNLFRCMGYIYCKDNLTRGKMLTTRDPAK---HESHGDSAILIVIS 313
 QY 89 HGRGEGFLKGEDEGMVKNLEFALNNKNCQALRAKPKYIIIOACRGQRDPGETV----- 143
 Db 314 HGEENVIIIGVDIPISTHEIYDLNNAANAPRLANKKIVFOACGGERDNGFPLDSVD 373
 QY 144 -----GGEIYVWITDSP-----OTIFTYDALHYSTVEGYTAJR 179
 Db 374 GVPAPFLRRGMWN-----RDGPLEFNLGCVRPQVOQWMEKPSQADILLIAYATTAQYVSWR 428
 QY 180 HDQKSGCFIQTLDVFT--KRKGHILELLETVTRRMAAEIYVQSG-KARKTNPEIQTSLR 214
 Db 429 NSAGSMFIOAVCEVFSHTAKMDVVELLITVNNKKYA 465

RESULT 12

B56084
 interleukin-1beta converting enzyme gamma isozyne - human
 C/Species: Homo sapiens (man)
 C/Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
 C/Accession: B56084
 R/Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
 J. Biol. Chem. 270, 4312-4317, 1995
 A/Title: Cloning and expression of four novel isoforms of human interleukin-1beta conver

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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:50:22 ; Search time 59.5 Seconds
(without alignments)
1268.642 Million cell updates/sec

Title: US-10-068-564-5

Perfect score: 1239
Sequence: 1 MSNPRSLSEKYMGSALAL.....KARKTNPISQTLRRYLQ 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239	100.0	242	9 US-09-989-903-5	Sequence 5, Appl1
2	1239	100.0	242	14 US-10-068-564-5	Sequence 5, Appl1
3	1234	99.6	242	9 US-09-845-028-2	Sequence 2, Appl1
4	1234	99.6	242	10 US-09-851-873-105	Sequence 105, App
5	1234	99.6	242	15 US-10-114-432-3	Sequence 3, Appl1
6	1234	99.6	242	15 US-10-114-432-15	Sequence 15, Appl1
7	1234	99.6	242	15 US-10-114-432-17	Sequence 17, Appl1
8	1234	99.6	242	15 US-10-114-432-18	Sequence 18, Appl1
9	1234	99.6	242	15 US-10-114-432-26	Sequence 26, Appl1
10	1234	99.6	242	15 US-10-114-432-27	Sequence 27, Appl1
11	1234	99.6	242	15 US-10-114-432-28	Sequence 28, Appl1
12	1234	99.6	242	15 US-10-114-432-30	Sequence 30, Appl1
13	1234	99.6	242	15 US-10-114-432-31	Sequence 31, Appl1
14	1234	99.6	242	15 US-10-114-432-67	Sequence 67, Appl1
15	1234	99.6	242	15 US-10-114-432-69	Sequence 69, Appl1

16	1234	99.6	242	15 US-10-114-432-71	Sequence 71, Appl1
17	1234	99.6	242	15 US-10-114-432-73	Sequence 73, Appl1
18	1232	99.4	242	15 US-10-114-432-13	Sequence 13, Appl1
19	1232	99.4	242	15 US-10-114-432-23	Sequence 23, Appl1
20	1229	99.2	241	15 US-10-114-432-37	Sequence 37, Appl1
21	1222	98.6	242	15 US-10-114-432-11	Sequence 11, Appl1
22	1222	98.6	242	15 US-10-114-432-22	Sequence 22, Appl1
23	1200	96.9	241	15 US-10-114-432-36	Sequence 36, Appl1
24	1200	96.9	321	15 US-10-114-432-21	Sequence 21, Appl1
25	1200	96.9	321	15 US-10-114-432-66	Sequence 66, Appl1
26	1200	96.9	321	15 US-10-114-432-72	Sequence 72, Appl1
27	1200	96.9	321	15 US-09-764-803A-24	Sequence 24, Appl1
28	1194	96.4	242	9 US-09-764-803A-9	Sequence 9, Appl1
29	1189	96.0	229	9 US-09-764-803A-4	Sequence 9, Appl1
30	1166	94.1	214	9 US-09-989-903-9	Sequence 9, Appl1
31	1065	86.0	214	14 US-10-068-564-9	Sequence 29, Appl1
32	1065	86.0	253	15 US-10-114-432-29	Sequence 2, Appl1
33	934.5	75.4	257	9 US-09-764-803A-2	Sequence 2, Appl1
34	934.5	75.4	260	14 US-10-068-564-2	Sequence 34, Appl1
35	934.5	75.4	260	14 US-10-114-432-34	Sequence 7, Appl1
36	890	71.8	230	9 US-09-989-903-7	Sequence 7, Appl1
37	890	71.8	230	14 US-10-068-564-7	Sequence 5, Appl1
38	890	71.8	230	15 US-10-114-432-5	Sequence 19, Appl1
39	890	71.8	230	15 US-10-114-432-19	Sequence 64, Appl1
40	890	71.8	230	15 US-10-114-432-68	Sequence 35, Appl1
41	890	71.8	230	15 US-10-114-432-35	Sequence 32, Appl1
42	890	71.8	230	15 US-10-114-432-32	
43	890	71.8	185	15 US-10-114-432-35	
44	686.5	55.4	134	15 US-10-114-432-32	
45	681	55.0	134	15 US-10-114-432-32	

ALIGNMENTS

RESULT 1
US-09-989-903-5
; Sequence 5, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemuri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-903-5

Query Match	100.0%	Score 1239	DB 9	Length 242
Best Local Similarity	100.0%	Pred. No. 1.3e-113	Indels 0	Gaps 0
Matches 242	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MSNPRSLSEKYMGSALALILCVTKARGSEEDLDALHMRQLRFESTMKRDPYAEQ	60	
DB	1	MSNPRSLSEKYMGSALALILCVTKARGSEEDLDALHMRQLRFESTMKRDPYAEQ	60	
QY	61	FOELEKFOQALDSREDPVSCAFVIMAHGREGLKGEDEMYKLELFEALNNKNOAL	120	
DB	61	FOELEKFOQALDSREDPVSCAFVIMAHGREGLKGEDEMYKLELFEALNNKNOAL	120	
QY	121	RARPKYITIDACGEQDPBETVGGDEIVWIDSPOTITPYDALHYSTVEGYIAYRH	180	
DB	121	RARPKYITIDACGEQDPBETVGGDEIVWIDSPOTITPYDALHYSTVEGYIAYRH	180	
QY	181	DOKGSCFIQTLVVFETKRGHIELLTVTRNAEAELVOEGARKTNPISQTLRRYLQ	240	
DB	181	DOKGSCFIQTLVVFETKRGHIELLTVTRNAEAELVOEGARKTNPISQTLRRYLQ	240	

Db 181 DKGSCFIOTLVDFVTKRGHILELLTEVTRMAAEELVOEGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
Db 241 LQ 242

RESULT 2

US-10-068-564-5
; Sequence 5, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:
; APPLICANT: Alnemir, Emed S.
; APPLICANT: Fernandez-Alnemir, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-068-564-5

Query Match 100.0%; Score 1239; DB 14; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;

Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMGSAALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPTAQ 60
Db 1 MSNPRLSEEEKYDMGSAALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPTAQ 60
QY 61 FOEELKEFQOALDSREDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120
Db 61 FOEELKEFQOALDSREDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIQACRGORDPGETVGDDEIWMVTKDSPQITPTTDLAHVYSTVEGYIAYRH 180
Db 121 RAKPKYIIQACRGORDPGETVGDDEIWMVTKDSPQITPTTDLAHVYSTVEGYIAYRH 180
QY 181 DKGSCFIOTLVDFVTKRGHILELLTEVTRMAAEELVOEGKARKTNPEIOSTLRKRLY 240
Db 181 DKGSCFIOTLVDFVTKRGHILELLTEVTRMAAEELVOEGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
Db 241 LQ 242

RESULT 3

US-09-845-028-2
; Sequence 2, Application US/09845028
; Patent No. US20020081705A1
; GENERAL INFORMATION:
; APPLICANT: Mankovich, John
; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
; FILE REFERENCE: BBI-111
; CURRENT APPLICATION NUMBER: US/09/845,028
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,962
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-028-2

Query Match 99.6%; Score 1234; DB 9; Length 242;

Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMGSAALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPTAQ 60
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Db 121 RAKPKYIIQACRGORDPGETVGDDEIWMVTKDSPQITPTTDLAHVYSTVEGYIAYRH 180
QY 181 DKGSCFIOTLVDFVTKRGHILELLTEVTRMAAEELVOEGKARKTNPEIOSTLRKRLY 240
Db 181 DKGSCFIOTLVDFVTKRGHILELLTEVTRMAAEELVOEGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
Db 241 LQ 242

RESULT 4

US-09-851-873-105
; Sequence 105, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kletzien, Rolf F
; APPLICANT: Reardon, Ilene M
; TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
; CURRENT APPLICATION NUMBER: US/09/851,873
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 105
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-851-873-105

Query Match 99.6%; Score 1234; DB 10; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYDMGSAALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPTAQ 60
Db 1 MSNPRLSEEEKYDMGSAALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPTAQ 60
QY 61 FOEELKEFQOALDSREDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120
Db 61 FOEELKEFQOALDSREDPVSCAFVILMAHGREGFLKGEDGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIQACRGORDPGETVGDDEIWMVTKDSPQITPTTDLAHVYSTVEGYIAYRH 180
Db 121 RAKPKYIIQACRGORDPGETVGDDEIWMVTKDSPQITPTTDLAHVYSTVEGYIAYRH 180
QY 181 DKGSCFIOTLVDFVTKRGHILELLTEVTRMAAEELVOEGKARKTNPEIOSTLRKRLY 240
Db 181 DKGSCFIOTLVDFVTKRGHILELLTEVTRMAAEELVOEGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
Db 241 LQ 242

RESULT 5

US-10-114-432-3
; Sequence 3, Application US/10114432
; Publication No. US20040019915A1

GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-3

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEBEKYMGSALALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPATAQ 60
DB 1 MSNPSLEBEKYMGSARLALLICVTKAREGSEEDLDALHMFRLRPESTMKRDPATAQ 60
QY 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIIOACRGQRDPGEIVGDEIVWIKOSPQIIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKYIIIOACRGQRDPGEIVGDEIVWIKOSPQIIPYTDALHYSTVEGYIAYRH 180
QY 181 DKGSCFIQTLVDVFTKRGHILELLEVTTRMAEALVQEGARKTNPEIOSTLRKRLY 240
DB 181 DKGSCFIQTLVDVFTKRGHILELLEVTTRMAEALVQEGARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

RESULT 6
US-10-114-432-15
Sequence 15, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:

APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-15

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEBEKYMGSALALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPATAQ 60
DB 1 MSNPSLEBEKYMGSARLALLICVTKAREGSEEDLDALHMFRLRPESTMKRDPATAQ 60
QY 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIIOACRGQRDPGEIVGDEIVWIKOSPQIIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKYIIIOACRGQRDPGEIVGDEIVWIKOSPQIIPYTDALHYSTVEGYIAYRH 180
QY 181 DKGSCFIQTLVDVFTKRGHILELLEVTTRMAEALVQEGARKTNPEIOSTLRKRLY 240
DB 181 DKGSCFIQTLVDVFTKRGHILELLEVTTRMAEALVQEGARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

RESULT 7
US-10-114-432-17
Sequence 17, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:

APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-17

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEBEKYMGSALALILCVTKAREGSEEDLDALHMFRLRPESTMKRDPATAQ 60
DB 1 MSNPSLEBEKYMGSARLALLICVTKAREGSEEDLDALHMFRLRPESTMKRDPATAQ 60
QY 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
DB 61 FOEELKFOAIDSREDPVSCAFVVLMAHGREGFLKGEDEGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIIOACRGQRDPGEIVGDEIVWIKOSPQIIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKYIIIOACRGQRDPGEIVGDEIVWIKOSPQIIPYTDALHYSTVEGYIAYRH 180
QY 181 DKGSCFIQTLVDVFTKRGHILELLEVTTRMAEALVQEGARKTNPEIOSTLRKRLY 240
DB 181 DKGSCFIQTLVDVFTKRGHILELLEVTTRMAEALVQEGARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

Db 241 LQ 242

RESULT 8
US-10-114-432-18
Sequence 18, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-2006.00
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-18

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLBEEKYKMSGALALILCVTKARSGSEEDLALHMFROLRFESTMKRDPTAEQ 60
DB 1 MSNPRSLBEEKYKMSGARLALILCVTKARSGSEEDLALHMFROLRFESTMKRDPTAEQ 60
QY 61 FOELEKFOQALDSREDPVSCAFVILMAHGREGLKGEDEGMVKLENLFEALNNKCOAL 120
DB 61 FOELEKFOQALDSREDPVSCAFVILMAHGREGLKGEDEGMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIIOACGGEORDPGEIVGDEIVWVVKDSPQTIPTYDALHVSIVSGYIAYRH 180
DB 121 RAKPKYIIIOACGGEORDPGEIVGDEIVWVVKDSPQTIPTYDALHVSIVSGYIAYRH 180
QY 181 DQKSGCFIOTLVDFPKRGHILLETVTYRMAEAEIVOGKARKTNPEIOSTLRKRLY 240
DB 181 DQKSGCFIOTLVDFPKRGHILLETVTYRMAEAEIVOGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

RESULT 9
US-10-114-432-26
Sequence 26, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-2006.00
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
US-10-114-432-26

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-26

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLBEEKYKMSGALALILCVTKARSGSEEDLALHMFROLRFESTMKRDPTAEQ 60
DB 1 MSNPRSLBEEKYKMSGARLALILCVTKARSGSEEDLALHMFROLRFESTMKRDPTAEQ 60
QY 61 FOELEKFOQALDSREDPVSCAFVILMAHGREGLKGEDEGMVKLENLFEALNNKCOAL 120
DB 61 FOELEKFOQALDSREDPVSCAFVILMAHGREGLKGEDEGMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIIOACGGEORDPGEIVGDEIVWVVKDSPQTIPTYDALHVSIVSGYIAYRH 180
DB 121 RAKPKYIIIOACGGEORDPGEIVGDEIVWVVKDSPQTIPTYDALHVSIVSGYIAYRH 180
QY 181 DQKSGCFIOTLVDFPKRGHILLETVTYRMAEAEIVOGKARKTNPEIOSTLRKRLY 240
DB 181 DQKSGCFIOTLVDFPKRGHILLETVTYRMAEAEIVOGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

RESULT 10
US-10-114-432-27
Sequence 27, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-2006.00
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-27

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLBEEKYKMSGALALILCVTKARSGSEEDLALHMFROLRFESTMKRDPTAEQ 60
DB 1 MSNPRSLBEEKYKMSGARLALILCVTKARSGSEEDLALHMFROLRFESTMKRDPTAEQ 60
QY 61 FOELEKFOQALDSREDPVSCAFVILMAHGREGLKGEDEGMVKLENLFEALNNKCOAL 120
DB 61 FOELEKFOQALDSREDPVSCAFVILMAHGREGLKGEDEGMVKLENLFEALNNKCOAL 120
QY 121 RAKPKYIIIOACGGEORDPGEIVGDEIVWVVKDSPQTIPTYDALHVSIVSGYIAYRH 180
DB 121 RAKPKYIIIOACGGEORDPGEIVGDEIVWVVKDSPQTIPTYDALHVSIVSGYIAYRH 180

QY 181 DQKSGCFIOTLVDFVTKRKHILLETVTTRMAEALVOEGKARKTNPEIQTIRKRLY 240
 DB 181 DQKSGCFIOTLVDFVTKRKHILLETVTTRMAEALVOEGKARKTNPEIQTIRKRLY 240
 QY 241 LQ 242
 DB 241 LQ 242

RESULT 11
 US-10-114-432-28
 ; Sequence 28, Application US/10114432
 ; Publication No. US20040019915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Robert K.
 ; APPLICANT: Ge, Mangmao
 ; APPLICANT: Jakobivits, Aya
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
 ; TITLE OF INVENTION: DETECTION OF CANCER
 ; FILE REFERENCE: 51158-20066.00
 ; CURRENT APPLICATION NUMBER: US/10/114,432
 ; CURRENT FILING DATE: 2002-04-01
 ; NUMBER OF SEQ ID NOS: 88
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 28
 ; LENGTH: 242
 ; TYPE: PRF
 ; ORGANISM: Homo Sapiens
 ; US-10-114-432-28

Query Match 99.6%; Score 1234; DB 15; Length 242;
 Best Local Similarity 99.6%; Pred. No. 4.1e-113;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLBEEKYMSGALALILCVTKARSGSEEDLDALHMFROLRPESTMKRDPPTAEQ 60
 DB 1 MSNPRSLBEEKYMSGALALILCVTKARSGSEEDLDALHMFROLRPESTMKRDPPTAEQ 60
 QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGEMVKLENTFEALNNKQCAL 120
 DB 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGEMVKLENTFEALNNKQCAL 120
 QY 121 RAKPKYVYIIQACRGORPDETVGDEIVMWIKDSPQTIPTDYLHVSTVEGYIAYRH 180
 DB 121 RAKPKYVYIIQACRGORPDETVGDEIVMWIKDSPQTIPTDYLHVSTVEGYIAYRH 180
 QY 181 DQKSGCFIOTLVDFVTKRKHILLETVTTRMAEALVOEGKARKTNPEIQTIRKRLY 240
 DB 181 DQKSGCFIOTLVDFVTKRKHILLETVTTRMAEALVOEGKARKTNPEIQTIRKRLY 240
 QY 241 LQ 242
 DB 241 LQ 242

RESULT 12
 US-10-114-432-30
 ; Sequence 30, Application US/10114432
 ; Publication No. US20040019915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Robert K.
 ; APPLICANT: Ge, Mangmao
 ; APPLICANT: Jakobivits, Aya

;; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ;; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
 ;; TITLE OF INVENTION: DETECTION OF CANCER
 ;; FILE REFERENCE: 51158-20066.00
 ;; CURRENT APPLICATION NUMBER: US/10/114,432
 ;; CURRENT FILING DATE: 2002-04-01
 ;; NUMBER OF SEQ ID NOS: 88
 ;; SOFTWARE: FastSeq for Windows Version 4.0
 ;; SEQ ID NO 30
 ;; LENGTH: 242
 ;; TYPE: PRF
 ;; ORGANISM: Homo Sapiens
 ; US-10-114-432-30

Query Match 99.6%; Score 1234; DB 15; Length 242;
 Best Local Similarity 99.6%; Pred. No. 4.1e-113;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLBEEKYMSGALALILCVTKARSGSEEDLDALHMFROLRPESTMKRDPPTAEQ 60
 DB 1 MSNPRSLBEEKYMSGALALILCVTKARSGSEEDLDALHMFROLRPESTMKRDPPTAEQ 60
 QY 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGEMVKLENTFEALNNKQCAL 120
 DB 61 FOEELKFOQAIDSREDPVSCAFVVLMAHGREGLKGEDEGEMVKLENTFEALNNKQCAL 120
 QY 121 RAKPKYVYIIQACRGORPDETVGDEIVMWIKDSPQTIPTDYLHVSTVEGYIAYRH 180
 DB 121 RAKPKYVYIIQACRGORPDETVGDEIVMWIKDSPQTIPTDYLHVSTVEGYIAYRH 180
 QY 181 DQKSGCFIOTLVDFVTKRKHILLETVTTRMAEALVOEGKARKTNPEIQTIRKRLY 240
 DB 181 DQKSGCFIOTLVDFVTKRKHILLETVTTRMAEALVOEGKARKTNPEIQTIRKRLY 240
 QY 241 LQ 242
 DB 241 LQ 242

RESULT 13
 US-10-114-432-31
 ; Sequence 31, Application US/10114432
 ; Publication No. US20040019915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chailita-Bid, Pia M.
 ; APPLICANT: Raitano, Arthur B.
 ; APPLICANT: Paris, Mary
 ; APPLICANT: Hubert, Rene S.
 ; APPLICANT: Morrison, Robert K.
 ; APPLICANT: Ge, Mangmao
 ; APPLICANT: Jakobivits, Aya
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
 ; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
 ; TITLE OF INVENTION: DETECTION OF CANCER
 ; FILE REFERENCE: 51158-20066.00
 ; CURRENT APPLICATION NUMBER: US/10/114,432
 ; CURRENT FILING DATE: 2002-04-01
 ; NUMBER OF SEQ ID NOS: 88
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 31
 ; LENGTH: 242
 ; TYPE: PRF
 ; ORGANISM: Homo Sapiens
 ; US-10-114-432-31

Query Match 99.6%; Score 1234; DB 15; Length 242;
 Best Local Similarity 99.6%; Pred. No. 4.1e-113;
 Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLBEEKYMSGALALILCVTKARSGSEEDLDALHMFROLRPESTMKRDPPTAEQ 60
 DB 1 MSNPRSLBEEKYMSGALALILCVTKARSGSEEDLDALHMFROLRPESTMKRDPPTAEQ 60

```

QY 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGEQRPGETVSGDEIWMVKDSPTIIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGEQRPGETVSGDEIWMVKDSPTIIPYTDALHYSTVEGYIAYRH 180
QY 181 DQKSGCFIQLTVDFVFKRKHILLETVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240
DB 181 DQKSGCFIQLTVDFVFKRKHILLETVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

```

RESULT 14

```

US-10-114-432-67
; Sequence 67, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobivics, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-2006.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 67
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-67

```

```

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MSNPRLSEEEKYMGSAALALILICVTKARBSSEEDLDALFHMFRQLRFESTMKRDPPTAQ 60
DB 1 MSNPRLSEEEKYMGSAALALILICVTKARBSSEEDLDALFHMFRQLRFESTMKRDPPTAQ 60
QY 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGEQRPGETVSGDEIWMVKDSPTIIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGEQRPGETVSGDEIWMVKDSPTIIPYTDALHYSTVEGYIAYRH 180
QY 181 DQKSGCFIQLTVDFVFKRKHILLETVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240
DB 181 DQKSGCFIQLTVDFVFKRKHILLETVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

```

```

RESULT 15
US-10-114-432-69
; Sequence 69, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobivics, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F1 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-2006.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 69
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-69

```

```

Query Match 99.6%; Score 1234; DB 15; Length 242;
Best Local Similarity 99.6%; Pred. No. 4.1e-113;
Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MSNPRLSEEEKYMGSAALALILICVTKARBSSEEDLDALFHMFRQLRFESTMKRDPPTAQ 60
DB 1 MSNPRLSEEEKYMGSAALALILICVTKARBSSEEDLDALFHMFRQLRFESTMKRDPPTAQ 60
QY 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEELKFOQALDSREDPVSCAFVVLMAHGREGLKGDGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGEQRPGETVSGDEIWMVKDSPTIIPYTDALHYSTVEGYIAYRH 180
DB 121 RAKPKVYIIQACRGEQRPGETVSGDEIWMVKDSPTIIPYTDALHYSTVEGYIAYRH 180
QY 181 DQKSGCFIQLTVDFVFKRKHILLETVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240
DB 181 DQKSGCFIQLTVDFVFKRKHILLETVTTRMAEALVQEGKARKTNPEIOSTLRKRLY 240
QY 241 LQ 242
DB 241 LQ 242

```

Search completed: July 12, 2004, 14:04:00
Job time : 60.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:39:36 / Search time 72 Seconds
(without alignments)
949.674 Million cell updates/sec

Title: US-10-068-564-5
Perfect score: 1239
Sequence: 1 MSNPRLSEEXYDMSGALA.....KARKTNPISQTLRRKLYLQ 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_29Jan04:*
2: geneseqp180s:*
3: geneseqp190s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	1234	99.6	242	3	AAY93214 Amino aci
2	1234	99.6	242	5	AAG77980 Full-leng
3	1189	96.0	242	5	AAG77984 Full-leng
4	1166	94.1	229	3	AAY68865 Amino aci
5	1065	86.0	214	3	AAY93216 Amino aci
6	934.5	75.4	257	3	AAY68864 Amino aci
7	934.5	75.4	281	3	AAM93592 Mouse cas
8	934.5	75.4	281	3	AAY93213 Amino aci
9	890	71.8	230	3	AAY93215 Amino aci
10	472.5	38.1	234	5	AAT72882 Human asp
11	472.5	38.1	398	5	ABG76499 DNA encod
12	295	23.8	452	5	ABH10110 Mouse cas
13	293	23.6	452	7	ADB79812 Rat caspa
14	293	23.6	452	7	ADB79812 Rat Prote
15	293	23.6	452	7	ADB63000 Rat Prote
16	289	23.3	435	2	AAR98462 Human int
17	289	23.3	435	2	AAR98462 Human int
18	289	23.3	435	2	AAR98462 Human int
19	289	23.3	435	2	AAR98462 Human int
20	289	23.3	435	2	AAR98462 Human int
21	289	23.3	435	2	AAR98462 Human int
22	289	23.3	435	2	AAR98462 Human int
23	289	23.3	435	2	AAR98462 Human int
24	289	23.3	435	2	AAR98462 Human int
25	289	23.3	435	2	AAR98462 Human int

26	289	23.3	441	3	AAB14253 Human Ich
27	280	22.6	245	4	AAB59579 Human cas
28	279.5	22.6	277	7	ADB63080 Rat Prote
29	278.5	22.5	277	2	AAW47089 Rat inter
30	276	22.3	261	4	AAE00610 Chimeric
31	275	22.2	435	3	AAB14262 Mutant hu
32	274.5	22.2	277	4	AAG78712 Pig caspa
33	273.5	22.1	249	3	AAB26763 Human cas
34	273.5	22.1	277	2	AAW00372 Apoptain C
35	273.5	22.1	277	2	AAW00372 Apoptain C
36	273.5	22.1	277	2	AAW00372 Apoptain C
37	273.5	22.1	277	2	AAW00372 Apoptain C
38	273.5	22.1	277	2	AAW00372 Apoptain C
39	273.5	22.1	277	2	AAW00372 Apoptain C
40	273.5	22.1	277	2	AAW00372 Apoptain C
41	273	22.0	457	4	AAW25766 Human pro
42	272.5	22.0	277	2	AAW16600 Apoptain C
43	272.5	22.0	277	2	AAW16600 Apoptain C
44	272.5	22.0	277	2	AAW16600 Apoptain C
45	272.5	22.0	277	2	AAW16600 Apoptain C

ALIGNMENTS

RESULT 1
ID AAY93214 standard; protein; 242 AA.

XX AAY93214;

XX 04-SEP-2000 (first entry)

XX Amino acid sequence of a human caspase-14.

XX Caspase-14; cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region /note= "large subunit"

XX Active-site 130..134

XX Cleavage-site 146..147

XX Region 147..242

XX /note= "small subunit"

XX W0200028047-A1.

XX 18-MAY-2000.

XX 29-OCT-1999; 99WO-US025523.

XX 06-NOV-1998; 98US-00187789.

XX (UYE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandez-Alnemri T;

XX WPI: 2000-376558/32.

XX N-PSDB: AAA15164.

XX Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.

XX Claim 13; Fig 7; 78pp; English.

The present sequence represents a human caspase-14 polypeptide. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of

CC apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
CC diseases and ischemic injury are treated by administering anti-caspase-14
CC antibodies. The antibody is useful for determining the presence or the
CC level of caspase-14 in tissue sample and also for the isolation of
CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotrimer formation and
CC therefore, apoptosis
XX

XX Sequence 242 AA;

Query Match 99.6%; Score 1234; DB 3; Length 242;
Best Local Similarity 99.6%; Pred. No. 1.5e-120;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEEEKYDMSGALALILCVTKARSGSEEDLDLEHMFQRLPESTMKDPTAEQ 60
Db 1 MSNPSLEEEKYDMSGALALILCVTKARSGSEEDLDLEHMFQRLPESTMKDPTAEQ 60
QY 61 FOELEKFOQALDSREDPVSCAFVYLMAGREGLKSGDGMVKLENI.FEALNNKNCQAL 120
Db 61 FOELEKFOQALDSREDPVSCAFVYLMAGREGLKSGDGMVKLENI.FEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGEORDPGETVGDEIVWYIKDSPQITPYTDALHYVSTVEGYIAYRH 180
Db 121 RAKPKVYIIQACRGEORDPGETVGDEIVWYIKDSPQITPYTDALHYVSTVEGYIAYRH 180
QY 181 DOKGSCFIQTLVDVFTFRKGHIIELELTVTRMAEALVDEGKARKTNPEIQTSLRKRLY 240
Db 181 DOKGSCFIQTLVDVFTFRKGHIIELELTVTRMAEALVDEGKARKTNPEIQTSLRKRLY 240
QY 241 LQ 242
Db 241 LQ 242

RESULT 2

AAG77980

ID AAG77980 standard; protein; 242 AA.

AC AAG77980;

DT 05-APR-2002 (first entry)

DE Full-length human caspase-14.

KW Human; caspase-14; anti-apoptotic; apoptosis.

XX Homo sapiens.

XX WO200181595-A2.

XX 01-NOV-2001.

XX 27-APR-2001; 2001WO-US013831.

XX 27-APR-2000; 2000US-0199962P.

XX (KNOL) KNOLL GMBH.

XX Mankovich JA;

XX WPI; 2002-041410/05.

XX N-PSDB; AAK98248.

PT Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.

PS Claim 20; Fig 1; 58pp; English.

CC The sequence represents the novel full-length human caspase-14 protein,
CC referred to as "Caspase-14 NEW" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino

CC acid sequence with MSNPSLE, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein
XX

XX Sequence 242 AA;

Query Match 99.6%; Score 1234; DB 5; Length 242;
Best Local Similarity 99.6%; Pred. No. 1.5e-120;

Matches 241; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEEEKYDMSGALALILCVTKARSGSEEDLDLEHMFQRLPESTMKDPTAEQ 60
Db 1 MSNPSLEEEKYDMSGALALILCVTKARSGSEEDLDLEHMFQRLPESTMKDPTAEQ 60
QY 61 FOELEKFOQALDSREDPVSCAFVYLMAGREGLKSGDGMVKLENI.FEALNNKNCQAL 120
Db 61 FOELEKFOQALDSREDPVSCAFVYLMAGREGLKSGDGMVKLENI.FEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGEORDPGETVGDEIVWYIKDSPQITPYTDALHYVSTVEGYIAYRH 180
Db 121 RAKPKVYIIQACRGEORDPGETVGDEIVWYIKDSPQITPYTDALHYVSTVEGYIAYRH 180
QY 181 DOKGSCFIQTLVDVFTFRKGHIIELELTVTRMAEALVDEGKARKTNPEIQTSLRKRLY 240
Db 181 DOKGSCFIQTLVDVFTFRKGHIIELELTVTRMAEALVDEGKARKTNPEIQTSLRKRLY 240
QY 241 LQ 242
Db 241 LQ 242

RESULT 3

AAG77984

ID AAG77984 standard; protein; 242 AA.

AC AAG77984;

DT 05-APR-2002 (first entry)

DE Full-length human caspase-14 old.

KW Human; caspase-14; anti-apoptotic; apoptosis.

XX Homo sapiens.

XX WO200181595-A2.

XX 01-NOV-2001.

XX 27-APR-2001; 2001WO-US013831.

XX 27-APR-2000; 2000US-0199962P.

XX (KNOL) KNOLL GMBH.

XX Mankovich JA;

XX WPI; 2002-041410/05.

PT Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.

XX Example; Fig 1; 58pp; English.

CC The sequence represents the full-length human caspase-14 protein,
 CC referred to as "caspase-14 OLP" in the specification. The invention
 CC relates to a novel isolated human caspase-14 protein comprising an amino
 CC acid sequence with MSNPSSLE, at its amino terminus. The caspase-14 of
 CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
 CC of caspase-14 activity. The polypeptide is useful for identifying a
 CC compound which is a modulator of human caspase-14 activity, and is also
 CC useful for identifying a compound which modulates the interaction of
 CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
 CC for isolating the protein by standard techniques, and for detecting
 CC caspase-14 to evaluate the abundance and expression pattern. The antibody
 CC is also useful for diagnostically monitoring protein levels in a tissue
 CC as a part of a clinical testing procedure. The polypeptide is useful as a
 CC protease to cleave substrates and for inducing apoptosis in cells, in
 CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
 CC assay to identify other proteins that interact with human caspase-14
 CC protein.

XX Sequence 242 AA;

Query Match 96.0%; Score 1189; DB 5; Length 242;
 Best Local Similarity 99.6%; Pred. No. 7.6e-116;
 Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 EKYDMSGALALILCTYKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQFQEELEKQ 69
 DB 10 EKYDMSGALALILCTYKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQFQEELEKQ 69
 QY 70 QALDSREDEPVSQAFVILMAHGRGFLKGEDGEVVKLENTFEALNNKCCALRAKPKVYII 129
 DB 70 QALDSREDEPVSQAFVILMAHGRGFLKGEDGEVVKLENTFEALNNKCCALRAKPKVYII 129
 QY 130 QACRGQRDPGETVGGDEIVMTIKDSPQITPTDYLHYVSTVEGYIAYRHQKSGSCFIQ 189
 DB 130 QACRGQRDPGETVGGDEIVMTIKDSPQITPTDYLHYVSTVEGYIAYRHQKSGSCFIQ 189
 QY 190 TLVDVFTTKRGHILELITEVTRMAEAEIVQEGKARKTNPDIQSTLRKRLYLQ 242
 DB 190 TLVDVFTTKRGHILELITEVTRMAEAEIVQEGKARKTNPDIQSTLRKRLYLQ 242

RESULT 4

AAV68865 standard; protein; 229 AA.

XX AAV68865;

DT 16-MAY-2000 (first entry)

DE Amino acid sequence of a human caspase-14 splice variant.

XX Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
 KM keratinisation; wound healing.

XX Homo sapiens.

PN W0200004169-A1.

XX 27-JAN-2000.

XX 12-JUL-1999; 99WO-EP004939.

XX 17-JUL-1998; 98EP-00202422.

XX (VIAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX Van De Craen M, Declercq W, Vandenaebale P, Fiers W;

XX WPI; 2000-182433/16.

XX N-PSDB; AAZ60684.

XX New murine and human caspase homologues useful for treating skin related
 PT disorders.

XX Claim 2; Page 53-54; 68pp; English.

CC The present sequence represents a human caspase-like polypeptide. The
 CC specification also describes a murine caspase-like polypeptide. Caspases
 CC are cysteinyl aspartate-specific proteinases which play a central role in
 CC apoptosis. The polypeptides of the invention are related to human and
 CC murine caspase-2 and human caspase-9, and possess all of the typical
 CC amino acids involved in catalysis, including the QACRG box, and contain
 CC no or only a very short prodomain. mRNA expression of the homologues of
 CC the invention is predominant in the skin. The caspase-like polypeptides
 CC are useful for treating human or animal diseases, such as skin diseases.
 CC They are also useful for screening for compounds that modulate its
 CC activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
 CC polypeptides and polynucleotides are useful for modulating
 CC keratinisation, for diagnosing and treating inappropriate wound healing

XX Sequence 229 AA;

Query Match 94.1%; Score 1166; DB 3; Length 229;
 Best Local Similarity 99.6%; Pred. No. 1.8e-113;
 Matches 228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 MCGALALILCTYKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQFQEELEKQ 73
 DB 1 MCGARLALLILCTYKAREGSEEDLDALHMFRLQRFESTMKRDPPTAEQFQEELEKQ 60
 QY 74 SREDPVSQAFVILMAHGRGFLKGEDGEVVKLENTFEALNNKCCALRAKPKVYIIQACR 133
 DB 61 SREDPVSQAFVILMAHGRGFLKGEDGEVVKLENTFEALNNKCCALRAKPKVYIIQACR 120
 QY 134 GEQRDPGETVGGDEIVMTIKDSPQITPTDYLHYVSTVEGYIAYRHQKSGSCFIQ 193
 DB 121 GEQRDPGETVGGDEIVMTIKDSPQITPTDYLHYVSTVEGYIAYRHQKSGSCFIQ 180
 QY 194 VFTKRGHILELITEVTRMAEAEIVQEGKARKTNPDIQSTLRKRLYLQ 242
 DB 181 VFTKRGHILELITEVTRMAEAEIVQEGKARKTNPDIQSTLRKRLYLQ 229

RESULT 5

AAV93216 standard; protein; 214 AA.

XX AAV93216;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of a human caspase-14 splice variant.

XX Caspase-14; cell death specific protease; apoptosis stimulator;
 KM apoptosis; AIDS; neurodegenerative disease; ischemic injury.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Active-site 102..106

PN W0200028047-A1.

XX 18-MAY-2000.

XX 29-OCT-1999; 99WO-US025523.

XX 06-NOV-1998; 98US-00187789.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Alnemri ES, Fernandez-Alnemri T;

DR WPI; 2000-376558/32.
 DR N-PSDB; AAL1516.
 XX
 PT Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.
 PT
 XX
 PS Claim 42; Fig 9; 78pp; English.
 XX
 CC The present sequence represents a human caspase-14 splice variant. The
 CC polypeptide is a cell death specific protease, and is an apoptosis
 CC stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
 CC -14 antibodies are useful for treating or reducing the severity of
 CC pathological conditions associated with increased or decreased levels of
 CC apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
 CC diseases and ischemic injury are treated by administering anti-caspase-14
 CC antibodies. The antibody is useful for determining the presence or the
 CC level of caspase-14 in tissue sample and also for the isolation of
 CC caspase-14 with apoptotic activity or in screening assay to identify an
 CC agent that inhibits heterodimer or heterotetramer formation and
 CC therefore, apoptosis
 CC
 XX Sequence 214 AA;
 SQ

Query Match 86.0%; Score 1065; DB 3; Length 214;
 Best Local Similarity 88.0%; Pred. No. 6.2e-103;
 Matches 213; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MSNPRSLSEEEKYDMSGALMLILCVTKARSGSEEDLALHMFQQLRPESTMRKDPYAEQ 60
 Db 1 MSNPRSLSEEEKYDMSGALMLILCVTKARSGSE----- 34
 QY 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDEGMVLENTLFEALNNKNCAL 120
 Db 35 --FELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDEGMVLENTLFEALNNKNCAL 92
 QY 121 RAKPKVYIIQACRGEQDPGEGTGVGBIIVWYIKDSPQTIPTTYDALHVSITVEGYIAYRH 180
 Db 93 RAKPKVYIIQACRGEQDPGEGTGVGBIIVWYIKDSPQTIPTTYDALHVSITVEGYIAYRH 152
 QY 181 DOKSGCFIQTIVDFVTRKGHILELTVTRMAEALVQEGARKTNPEIOSTRKELY 240
 Db 153 DOKSGCFIQTIVDFVTRKGHILELTVTRMAEALVQEGARKTNPEIOSTRKELY 212
 QY 241 LQ 242
 Db 213 LQ 214

RESULT 6
 AAY68864
 ID AAY68864 standard; protein; 257 AA.
 XX
 AC AAY68864;
 XX
 DT 16-MAY-2000 (first entry)
 XX
 DE Amino acid sequence of a murine caspase-like polypeptide.
 XX
 KW Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
 KW keratinisation; wound healing.
 XX
 OS Mus musculus.
 XX
 PN WO200004169-A1.
 XX
 PD 27-JAN-2000.
 XX
 PF 12-JUL-1999; 99MO-EP004939.
 XX
 PR 17-JUL-1998; 98EP-0020422.
 XX
 PA (VLA--) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX

PI Van De Craen M, Declercq W, Vandenaebiele P, Fiers W;
 XX
 DR WPI; 2000-182433/16.
 DR N-PSDB; AAZ60683.
 XX
 PT New murine and human caspase homologues useful for treating skin related
 PT disorders.
 XX
 PS Claim 1; Page 51-52; 68pp; English.
 XX
 CC The present sequence represents a murine caspase-like polypeptide. The
 CC specification also describes a human caspase-like polypeptide. Caspases
 CC are cysteine1 aspartate-specific proteinases which play a central role in
 CC apoptosis. The polypeptides of the invention are related to human and
 CC murine caspase-2 and human caspase-9, and possess all of the typical
 CC amino acids involved in catalysis, including the QACRG box, and contain
 CC no or only a very short prodomain. mRNA expression of the homologues of
 CC the invention is predominant in the skin. The caspase-like polypeptides
 CC are useful for treating human or animal diseases, such as skin diseases.
 CC They are also useful for screening for compounds that modulate its
 CC activity, i.e. agonists, antagonists, and inhibitors.
 CC CC polynucleotides and polynucleotides are useful for modulating
 CC keratinisation, for diagnosing and treating inappropriate wound healing
 CC
 XX Sequence 257 AA;
 SQ

Query Match 75.4%; Score 934.5; DB 3; Length 257;
 Best Local Similarity 70.9%; Pred. No. 3.8e-89;
 Matches 180; Conservative 31; Mismatches 30; Indels 13; Gaps 2;

QY 1 MSNPRSLSEEEKYDMSGALMLILCVTKARSGSEEDLALHMFQQLRPESTMRKDPYAEQ 60
 Db 5 MSNPQPLSEEEKYDMSGALMLILCVTKARSGSEEDLALHMFQQLRPESTMRKDPYAEQ 64
 QY 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDEGMVLENTLFEALNNKNCAL 120
 Db 65 FLELEDFEQQTINWEPVSCAFVVLMAHGREGFLKGEDEGMVLENTLFEALNNKNCAL 124
 QY 121 RAKPKVYIIQACRGEQDPG-----ETVSGDEIIVWYIKDSPQTIPTTYDALHV 168
 Db 125 RAKPKVYIIQACRGEQDPGELRGNEELGDELDGDE--VAVLKNNPQSIPTTYDTLHI 183
 QY 169 YSTVEGYIAYRHQKSGCFIQTIVDFVTRKGHILELTVTRMAEALVQEGARKTN 228
 Db 184 YSTVEGYIAYRHQKSGCFIQTIVDFVTRKGHILELTVTRMAEALVQEGARKTN 243
 QY 229 PEIOSTRKRLYDQ 242
 Db 244 PEVQSTLRKKLYIQ 257

RESULT 7
 AAW93592
 ID AAW93592 standard; protein; 281 AA.
 XX
 AC AAW93592;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Mouse caspase-14 protein.
 XX
 KW Caspase-14; murine; protease; treatment; apoptotic-related disease;
 KW autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS;
 KW neurodegenerative disease; ischemic injury; anti-idiotypic antibody;
 KW caspase-14 processing activity; epitope; competitor; modulator.
 XX
 OS Mus sp.
 XX
 PN WO9910504-A2.
 XX
 PD 04-MAR-1999.
 XX
 PF 26-AUG-1998; 98MO-US017715.
 XX

OY	169	YSTVSGYLAYRRDOKSGCICITLVYFETRKGHIIELLVEVTRRMAEALVDEGKARKN	228
	203	YSTVSGYLSYRDEKOSGFIQTLDVFIHKKGSIFELTEITRLTMANTVEWDEGKPRKN	262
OY	229	PRIGSTLRRLYLQ	242
Db	263	PEVOSTLRKKLYLQ	276

RESULT 9
AAV93215
ID AAV93215 standard; protein; 230 AA.

Amino acid sequence of a human caspase-14 splice variant.

KM Caspase-14; cell death specific protease; apoptosis stimulator;
KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.
VV

OS Homo sapiens.

	Key	Location/Qualifiers
FH	Active-site	130. .134
FT		

PN WO200028047-A1.

PD 18-MAY-2000.

PF 29-OCT-1999; 99WO-US025523.

PR 06-NOV-1998; 98US-00187789.

PA (UYJE-) UNIV JEFFERSON THOMAS.

PI Alnemri ES, Fernandez-Alnemri T;

DR WPI; 2000-376558/32.

DR N-PSDB; AAA15165.

PT Novel nuclear acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.

PS Claim 41; Fig 8; 78pp; English.

The present sequence represents a human caspase-14 splice variant. The polypeptide is a cell death specific protease, and is an apoptotic stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence or the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an agent that inhibits heterodimer or heterotetramer formation and therefore, apoptosis

Sequence 230 AA;

Query Match	71.8%	Score 830;	DB 3;	Length 230;
Best Local Similarity	99.4%	Pred. No. 1,5e-84;		
Matches 173; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

[illegible][illegible]

RESULT 10
AAU72882
ID AAU72882 standard; protein; 234 AA

Human aspartyl protease partial protein sequence #7.

KM Human; protease; PCR primer; cytosollic; immunomodulator; cardiant;
KM antitumor; antimitogenic; analgesic; endocrine; nocitropic; tranquiliser;
KM hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;
KM metalloproteinase; aspartyl protease; haematopoietic; breast; colon;
KM metalloproteinase; serine protease; cancer; haematopoietic; breast; colon;
KM lung; prostate; cervical; brain; ovarian; bladder; kidney; pain;
KM immune-related disease; cardiovascular disease; neuronal disease;
KM migraine; sexual dysfunction; mood disorder; attention disorder;
KM cognition disorder; hypotension; hypertension; psychotic disorder;
KM dyskinnesia; metabolic disorder; inflammatory disorder

OS Homo sapiens.

PN W0200183782-A2

PD 08-NOV-2001

PF 04-MAY-2001; 2001WO-US014431.

PR 04-MAY-2000; 2000US-0201879P.

PA (SUGE-) SUGEN INC.

PI Plowman GD, whyte D, Sudarsanam S, Manning G, Caenepeel S;

Payne V;

DR WPI; 2002-041502/05.

DR N-PSDB; AAS97165.
XX

PT Novel protease polypeptide useful for screening for substances that may
PT be used to treat, e.g., cancers, immune-related diseases, cardiovascular
PT disease, migraine, pain, psychotic and inflammatory disorders.
XX
XX Claim 28; Fig 2A; 232PP; English.
XS

PS Claim 28; Fig 2A; 232pp; English.

The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues of blood or haematopoietic origin, of the breast, colon, lung, prostate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders), attention disorders, cognition disorders, hypertension, hyperextension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAU2876-AAU72910 represent human protease amino acid sequences of the invention

Sequence 234 AA;

Query Match	38.1%;	Score 472.5;	DB 5;	Length 234;
Best Local Similarity	45.0%;	Pred. No. 8.1e-41;		
Matches 107; Conservative	47;	Mismatches 73;	Indels 11;	Gaps 7;

PA (ISIS-) ISIS PHARM INC.
 XX Zhang H, Walt AT;
 XX WPI; 2002-351998/38.
 DR N-PSDB; ABB58563.
 XX
 PT New antisense compounds targeted to nucleic acid molecule encoding
 PT caspase 2, useful for treating diseases or conditions associated with
 PT neurodegenerative diseases.
 PS Example 13; Page 111-113; 146pp; English.
 XX
 CC The invention relates to a compound 8-50 nucleobases in length targeted
 CC to a nucleic acid molecule encoding caspase 2, which specifically
 CC hybridizes with and inhibits the expression of caspase 2, or specifically
 CC hybridizes with at least an 8-nucleobase portion of an active site on a
 CC nucleic acid molecule encoding caspase 2. The activity of antisense
 CC oligonucleotides of the invention may be described as, cytostatic,
 CC osteopathic, cerebroprotective, neuroprotective, antileptic,
 CC antiinflammatory and antimicrobial. The antisense compounds are useful
 CC for treating an animal having a disease or condition associated with
 CC caspase 2, such as haematopoietic disorder, bone metabolism disorder,
 CC cholesterol disorder, or a hyperproliferative disorder. These compounds
 CC may further be used as research reagents and diagnostics, to distinguish
 CC between functions of various members of a biological pathway, in the
 CC treatment of a disease or disorder which can be treated by modulating the
 CC expression of caspase 2, including cancer, blood disorders, stroke, brain
 CC injury and neurodegenerative diseases. They may also be used for
 CC prophylaxis, e.g. to prevent or delay infection, inflammation or tumour
 CC formation. The current sequence represents the mouse caspase 2 protein
 XX
 SQ Sequence 452 AA;
 Query Match 23.8%; Score 295; DB 5; Length 452;
 Best Local Similarity 31.5%; Pred. No. 8.2e-22;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;
 QY 29 REGSEEDLALHEMFROLPESTMKRDPFAEQOELEKFOAIDSREDPVSCAFVYMA 88
 Db 219 RSGGDVHTLTVLTKLGYNAVHVDQTAQEMQKLNFAQ-LPAHRTDSCV-VALLS 276
 QY 89 HGESEGLKEDGEMVLENI.FEALNNKNCQALAKKPVYIIQACRGDRDPG----- 140
 Db 277 HGEVGGIYGVDGKLLDQEVFRFLFDNANCPSLQNKPKMFPFIQACRGDETDRGVDDQDGN 336
 QY 141 -----ETVGGDEIVMVIKSPQITPTTDALHYSTVEGYIAYRHQDGSCTIQTIV 192
 Db 337 HTQSPGCESSDAKKEELMKR-----LPTKSDMICGACIKGNAAAMNTRKGSWYTEALT 391
 QY 193 DVFTK-KGHILELLTEVTRMAEALVQEGARKTN-----PEIQSTLKRRLYL 241
 Db 392 QVFSEBACMHWADMLVKYNALIKE-----REGYAPGTEFHRCKEMSEYCSITLCOQLYL 445
 RESULT 13
 ADB79812
 ID ADB79812 standard; protein; 452 AA.
 XX
 AC ADB79812;
 XX
 XX 04-DEC-2003 (first entry)
 DT
 DE Rat caspase 2, Ich-1, SEQ ID 52.
 XX
 KW Analgesic; pain; streptozocin-induced diabetes; rat.
 XX
 OS Rattus norvegicus.
 XX
 PN EPI279744-A2.
 XX
 PD 29-JAN-2003.

XX
 PF 26-JUL-2002; 2002EP-00255249.
 XX
 PR 27-JUL-2001; 2001GB-00018354.
 XX
 PR 07-FEB-2002; 2002GB-00002910.
 XX
 PA (WARN) WARNER LAMBERT CO.
 PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
 XX WPI; 2003-395407/38.
 DR N-PSDB; ADB79813.
 XX
 PT Use of isolated gene sequences and encoded polypeptides that are
 PT upregulated in the spinal cord in response to streptozocin-induced
 PT diabetes for screening compounds for the treatment of pain, or for
 PT diagnosing pain.
 XX
 PS Claim 1; Page 115-117; 334pp; English.
 CC The present invention relates to nucleotide sequences which are useful in
 CC the screening of compounds for the treatment of pain, or for the
 CC diagnosis of pain. The nucleotide sequences are up-regulated in the
 CC spinal cord in response to streptozocin-induced diabetes. The present
 CC sequence was used to illustrate the invention.
 XX
 SQ Sequence 452 AA;
 Query Match 23.6%; Score 293; DB 7; Length 452;
 Best Local Similarity 31.5%; Pred. No. 1.3e-21;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;
 QY 29 REGSEEDLALHEMFROLPESTMKRDPFAEQOELEKFOAIDSREDPVSCAFVYMA 88
 Db 219 RSGGDVHTLTVLTKLGYNAVHVDQTAQEMQKLNFAQ-LPAHRTDSC-IVALLS 276
 QY 89 HGESEGLKEDGEMVLENI.FEALNNKNCQALAKKPVYIIQACRGDRDPG----- 140
 Db 277 HGEVGGIYGVDGKLLDQEVFRFLFDNANCPSLQNKPKMFPFIQACRGDETDRGVDDQDGN 336
 QY 141 -----ETVGGDEIVMVIKSPQITPTTDALHYSTVEGYIAYRHQDGSCTIQTIV 192
 Db 337 HAQSPGCESSDAKKEELMKR-----LPTKSDMICGACIKGNAAAMNTRKGSWYTEALT 391
 QY 193 DVFTK-KGHILELLTEVTRMAEALVQEGARKTN-----PEIQSTLKRRLYL 241
 Db 392 QVFSEBACMHWADMLVKYNALIKE-----REGYAPGTEFHRCKEMSEYCSITLCOQLYL 445
 RESULT 14
 ADE63000
 ID ADE63000 standard; protein; 452 AA.
 XX
 AC ADE63000;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 DE Rat Protein AAB96379, SEQ ID NO 8934.
 XX
 KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 OS Rattus norvegicus.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002MO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.

XX (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI, 2003-268312/26.
 DR GENBANK; AAB96379.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

Claim 1, Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPD at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 452 AA;

Query Match 23.6%; Score 293; DB 7; Length 452;
 Best Local Similarity 31.5%; Pred. No. 1.3e-21;
 Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY 29 REGSEBDLALHEMFRLRFESTMKRDPPTAEQFOEIEKEFOAIDSREDPVSCAFVYVMA 88
 DB 219 RSGGDVDTLTLVTLFKLGVNHYLVDTAQEMQEKLNFAQ-LPAHRTVDSCLVALIS 276
 QY 89 HGREGFLKGEDEGMVTKLENLFEALNNKNCQALPAKRVYITQCRGEORPQ----- 140
 DB 277 HGEVGGIYGVGDKILOEVFRLFDNANCPSLQNKRMFFIQCRGDETRGVDDQDGKN 336
 QY 141 -----ETVGGDEIYMWIKDSPQITPTDALHYVSTVEGYTAVRHDKGSCFIQTLV 192
 DB 337 HAQSPGCEBSDAQEELMKR-----LPTSDMICGACLKGNAMNMTKRGSMYIDALT 391
 QY 193 DVFTKR--KGHIIELETVTRMAEALVOEGARKTN-----PIQSTLRKRYL 241
 DB 392 QVFERACDHNHADMVKNVALLKE-----REGVAPGTEFHRCKEMSEYCSITLCOQILY 445

RESULT 15

AA66771
 ID AAR6771 standard; protein; 435 AA.

XX AAR6771;

XX 25-MAR-2003 (revised)
 DT 13-SEP-1995 (first entry)

XX Human interleukin-1 beta converting enzyme ced 3 homolog Ich-1(L).
 DE
 XX Human interleukin-1 beta converting enzyme ced 3 homolog; Ich-1(L);
 KW oncogene bcl-2; programmed cell death; cancer treatment.
 KM
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Active-site 301..305
 FT
 PN WO9500160-A1.
 XX
 XX 05-JAN-1995.
 XX
 XX 10-JUN-1994; 94WO-US006630.
 XX PF
 XX 24-JUN-1993; 93US-00080850.
 XX PR
 XX (GHEO) GEN HOSPITAL CORP.
 XX
 XX Yuan J, Mura M;
 PI
 XX WPI: 1995-051742/07.
 DR N-PSDB; AAQ79971.
 XX
 XX or preventing programmed cell death in vertebrate cells - by inhibiting
 PT the activity of interleukin-1 beta converting enzyme.
 PS Example 5; Fig 12A; 116pp; English.

XX AAQ79971 encodes AAR6771 human interleukin-1 beta converting enzyme ced
 CC 3 homolog Ich-1(L), increasing Ich-1(L)'s enzymatic activity can promote
 CC the programmed cell death of cancer cells (pref. those overexpressing the
 CC bcl-2 oncogene), this can be used as the basis of a new cancer treatment.
 CC Alternatively by reducing Ich-1(L)'s enzymatic activity programmed cell
 CC death can be inhibited, this may be useful in the development of new cell
 CC lines which remain viable in culture for extended or indefinite periods,
 CC independent of growth factors. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 XX Sequence 435 AA;

Query Match 23.3%; Score 289; DB 2; Length 435;
 Best Local Similarity 31.1%; Pred. No. 3.3e-21;
 Matches 74; Conservative 51; Mismatches 77; Indels 36; Gaps 7;

QY 29 REGSEBDLALHEMFRLRFESTMKRDPPTAEQFOEIEKEFOAIDSREDPVSCAFVYVMA 88
 DB 202 RSGGDVDTLTLVTLFKLGVNHYLVDTAQEMQEKLNFAQ-LPAHRTVDSCLVALIS 259
 QY 89 HGREGFLKGEDEGMVTKLENLFEALNNKNCQALPAKRVYITQCRGEORPQ----- 140
 DB 260 HGEVGGIYGVGDKILOEVFRLFDNANCPSLQNKRMFFIQCRGDETRGVDDQDGKN 319
 QY 141 -----ETVGGDEIYMWIKDSPQITPTDALHYVSTVEGYTAVRHDKGSCFIQTLV 192
 DB 320 HAQSPGCEBSDAQE-----LPTSDMICGACLKGNAMNMTKRGSMYIDALT 374
 QY 193 DVFTKR--KGHIIELETVTRMAEALVOEGARKTN-----PIQSTLRKRYL 241
 DB 375 QVFERACDHNHADMVKNVALLKE-----REGVAPGTEFHRCKEMSEYCSITLCHILY 428

Search completed: July 12, 2004, 13:47:46
 Job time : 74 secs

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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:43:31 ; Search time 49.5 Seconds
(without alignments)
1542.533 Million cell updates/sec

Title: US-10-068-564-5
Perfect score: 1239
Sequence: 1 MSNPSRLEEKYDMSCALAA.....KARKTNPETQSTIRKRLYLQ 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMHL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mmc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	298	24.1	452	11	Q8C9H7 mus musculus
2	295	23.8	452	11	Q8K241 mus musculus
3	293	23.6	452	11	O55194 rat mus musculus
4	289.5	23.4	423	13	Q91B67 xenopus lae
5	289	23.3	435	4	Q9BUP7 homo sapien
6	284.5	22.6	283	13	Q93417 gallus gall
7	279.5	22.6	316	5	Q817B0 geodia cydo
8	279.5	22.6	426	5	O81672 geodia cydo
9	275.5	22.2	277	6	O8MUC3 oryctolagus
10	275.5	22.2	277	6	O8MUC1 felis silve
11	274.5	22.2	277	6	Q95ND5 sus scrofa
12	274.5	22.2	383	13	Q919L7 brachydanio
13	273.5	22.1	313	11	Q8CHV5 mus musculus
14	272.5	22.0	277	6	O8MKI5 canis famli
15	272	22.0	399	13	Q91B63 xenopus lae
16	270	21.8	303	11	O88550 rat mus musculus

17	269.5	21.8	452	11	Q9R0T0 mus musculus
18	269	21.7	482	13	Q90WT1 mus musculus
19	266.5	21.5	282	13	Q98U18 brachydanio
20	264.5	21.3	290	13	Q81S8 oryzias lat
21	263.5	21.3	453	11	O8C3Q0 mus musculus
22	263.5	21.3	454	11	O8C3Q9 mus musculus
23	261.5	21.1	289	5	Q86F10 anopheles s
24	260.5	21.0	403	13	Q90WU0 gallus gall
25	257	20.7	476	13	Q91B73 brachydanio
26	256	20.7	500	13	Q91B64 xenopus lae
27	256	20.7	520	13	Q91B62 xenopus lae
28	255	20.6	417	5	Q9YIU6 pristinonchu
29	254.5	20.5	454	11	Q9JHK1 ractus norv
30	250.5	20.2	280	13	Q80GW9 fuqua rubrip
31	250.5	20.2	318	13	Q91B65 xenopus lae
32	249.5	20.1	280	13	O8G442 fuqua rubrip
33	248	20.0	522	4	O81UP5 fuqua rubrip
34	242.5	19.6	189	11	O8BNT4 homo sapien
35	242.5	19.6	276	11	O9D089 mus musculus
36	242.5	19.6	280	13	O81S9 oryzias lat
37	241.5	19.5	276	11	Q99M47 mus musculus
38	239.5	19.3	293	5	O819V7 bombyx mori
39	236.5	19.1	299	5	O81955 spodoptera
40	235.5	19.0	182	6	O77623 ovis aries
41	235	19.0	277	11	O35397 ractus norv
42	232.5	18.8	328	5	O81TP3 brachydanio
43	230.5	18.6	482	11	Q9JHX4 ractus norv
44	228.5	18.4	347	5	Q9GV89 hydra atten
45	228.5	18.4	404	13	Q9DDJ2 brachydanio

ALIGNMENTS

RESULT 1
ID Q8C9H7 PRELIMINARY; PRT; 452 AA.
AC Q8C9H7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 2.
GN CASP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=2354683; PubMed=1246851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK042072; BAC3153.1; -
DR MGD; MGI:97295; Casp2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; F:apoptosis; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PRO0376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CARD; 1.
DR PROSITE; PSS0209; CARD; 1.

DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50689 MW; C3715908508619CA CRC64;

Query Match 24.1%; Score 298; DB 11; Length 452;
Best Local Similarity 31.9%; Pred. No. 5.8e-17;
Matches 76; Conservative 51; Mismatches 75; Indels 36; Gaps 7;

QY 29 REGSEEDLALHMFROLPFESTMKRDPPTAEOFOEELKEFOQALDSREDPVSCAFVYMA 88
DB 219 RSGGDVHTTLVTLFRLGYNVHLHDQTAQEMQKLNFAQ-LPAHRTVDSQV-VALLS 276
QY 89 HGRGFLKGEDEGVNKLLENFEALNNKNCQALRAKPVYIIQAQGRGDRPG----- 140
DB 277 HGVGGIYGVGDKLLQQLQEVFRLFDNANCPSLQNKPKPMFFIQAQGRGETRGVDQDGKN 336
QY 141 -----ETVGGDEIYMWIKDSPQITPTVDALHYSTVGGYTAHYHDKGSCFIQTIV 192
DB 337 HTQSPGCEESDAGEELMKR-----LPTSDMTCGYACIKGNAMNTRKGSWYIALT 391
QY 193 DVFTKR--KHILLELLEVTNRMAEALVQEGKARKTN-----PEIQTTRRRYVL 241
DB 392 QVFSERACDWHVADMVKNVALLKE----REGYAPGTEFHRCKEMSEYCSITLCOQLYL 445

RESULT 2

Q8K241 PRELIMINARY; PRT; 452 AA.
AC Q8K241;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 2.
GN CASP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034262; AAH34262.1; -.
DR MGI; MGI:97295; Casp2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; CARD.
DR InterPro; IPR001309; ICE_P10.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASG; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50661 MW; A4DE25A712PAB855 CRC64;

Query Match 23.8%; Score 295; DB 11; Length 452;
Best Local Similarity 31.5%; Pred. No. 1e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY 29 REGSEEDLALHMFROLPFESTMKRDPPTAEOFOEELKEFOQALDSREDPVSCAFVYMA 88
DB 219 RSGGDVHTTLVTLFRLGYNVHLHDQTAQEMQKLNFAQ-LPAHRTVDSQV-VALLS 276
QY 89 HGRGFLKGEDEGVNKLLENFEALNNKNCQALRAKPVYIIQAQGRGDRPG----- 140

DB 219 RSGGDVHTTLVTLFRLGYNVHLHDQTAQEMQKLNFAQ-LPAHRTVDSQV-VALLS 276
QY 89 HGRGFLKGEDEGVNKLLENFEALNNKNCQALRAKPVYIIQAQGRGDRPG----- 140
DB 277 HGVGGIYGVGDKLLQQLQEVFRLFDNANCPSLQNKPKPMFFIQAQGRGETRGVDQDGKN 336
QY 141 -----ETVGGDEIYMWIKDSPQITPTVDALHYSTVGGYTAHYHDKGSCFIQTIV 192
DB 337 HTQSPGCEESDAGEELMKR-----LPTSDMTCGYACIKGNAMNTRKGSWYIALT 391

QY 193 DVFTKR--KHILLELLEVTNRMAEALVQEGKARKTN-----PEIQTTRRRYVL 241
DB 392 QVFSERACDWHVADMVKNVALLKE----REGYAPGTEFHRCKEMSEYCSITLCOQLYL 445

RESULT 3

ID 055194 PRELIMINARY; PRT; 452 AA.
AC 055194;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NEDD2/ICH-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98087427; PubMed=9427555;
RA Sato N., Milligan C.E., Uchiyama Y., Oppenheim R.W.;
RT "Cloning and expression of the cDNA encoding rat caspase-2.";
RL Gene 202:127-132(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SEPRAGUE-DAMLEY; TISSUE=Brain;
RA Jin K.L., Simon R.P., Graham S.H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U77933; AAB96379.1; -.
DR EMBL; AF136231; AAD33684.1; -.
DR HSP; P29466; 1ICE.
DR HSP; P29466; 1ICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; CARD.
DR InterPro; IPR001309; ICE_P10.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASG; 1.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50728 MW; 03F9D096BB741CE3 CRC64;

Query Match 23.6%; Score 293; DB 11; Length 452;
Best Local Similarity 31.5%; Pred. No. 1.5e-16;
Matches 75; Conservative 52; Mismatches 75; Indels 36; Gaps 7;

QY 29 REGSEEDLALHMFROLPFESTMKRDPPTAEOFOEELKEFOQALDSREDPVSCAFVYMA 88
DB 219 RSGGDVHTTLVTLFRLGYNVHLHDQTAQEMQKLNFAQ-LPAHRTVDSQV-VALLS 276
QY 89 HGRGFLKGEDEGVNKLLENFEALNNKNCQALRAKPVYIIQAQGRGDRPG----- 140

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Db    277 HGVGGIGYGVNDGKLLQJGEVFRLPFNMANCPISLQNKPKEFIIQACKGDETDGDQQDKN   336
Qy    141 -----EIVGGDEIWMWIKDSFOPTITTYDIALHVSIVTBESYAIARHDQKSGCITQLTV   192
Db    337 HAQSPGCSESDAGKEELMKMR-----LEPSSMDTCGAALCKNGAMRNTKGSWIETALT   391
Qy    193 DVFKRK--KHGHILBELTEVTIRMAAEIVQEGSKAKTN-----PEIQSTLRKLYL      241
Db    392 QVESERACDMHWADWLVRNALIKE---REGYAFGETFHRCCKEMSEBVCSTLCQOYL      445

RESULT 4
091B67 PRELIMINARY; PRT; 423 AA.
Ac    091B67?
Dt    01-OCT-2000 (TREMBLrel. 15, Created)
Dt    01-OCT-2000 (TREMBLrel. 15, Last sequence update)
Dt    01-OCT-2003 (TREMBLrel. 25, Last annotation update)
De    Caspase-2.
GN     XCASPASE-2.
OS     Xenopus laevis (African clawed frog).
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC     Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC     Xenopodinae; Xenopus.
CX     NCBI_TaxID=8355;
RX     (1)
RP     SEQUENCE FROM N.A.
PX     MEDLINE=20209426; PubMed=10744739;
RA     Nakajima K., Takahashi A., Yaoita Y.;
RT     "Structure, expression and function of the Xenopus laevis caspase
family.";
RU     J. Biol. Chem. 275:10484-10491(2000).
DR     EMBL; AB038168; BAA94746.1; -.
DR     HSSP; P29466; IICE.
DR     MEROPS; C14.006; -.
DR     GO; GO:0005622; C:intracellular; IEA.
DR     GO; GO:10016328; F:apoptosis regulator activity; IEA.
DR     GO; GO:10030693; F:caspase activity; IEA.
DR     GO; GO:0006915; P:apoptosis; IEA.
DR     GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR     InterPro; IPRO01315; CARD.
DR     InterPro; IPRO02138; ICE_p10.
DR     InterPro; IPRO01309; ICE_p20.
DR     InterPro; IPRO02398; Peptidase_C14.
DR     Pfam; PF00619; CARD; 1.
DR     Pfam; PF00656; Peptidase_C14; 1.
DR     PRINTS; PR00376; ILIHCBENZME.
DR     SMART; SM00114; CARD; 1.
DR     SMART; SM00115; CASc; 1.
DR     PROSITE; PS50209; CARD; 1.
DR     PROSITE; PS01122; CASPAGE_CYS; 1.
DR     PROSITE; PS01121; CASPAGE_HIS; 1.
DR     PROSITE; PS50207; CASPAGE_P10; 1.
DR     PROSITE; PS50208; CASPAGE_P20; 1.
SQ     SEQUENCE 423 AA; 47123 MW; E91EBLFDI33F01FD CRC64;

Query Match          23.4%; Score 289.5; DB 13; Length 423;
Best Local Similarity 30.5%; Pred. No. 2,8e-16;
Matches 74; Conservative 51; Mismatches 71; Indels 47; Gaps 7

Qy    29 REGSEDDULALEHMFRQLRFESTMKNKDPTLAEOFOEELEKF-----QQAIDSREDPVSCAF   83
Db    187 RCGGGEVDVLASTLKFESSLIGYQVDAVRCNLNNAQSMMSLGAFSAFLPYHSADS-----CV   239
Qy    84 VTLMHGREGRGLKGEDEVKLKENIFEAANNKCQALKRAPKYLIIOACRGEDRDPG----        140
Db    240 VALTSHLDGAVAYGTDGKVVOLEVFATLDNAHCIPOLQNKKPKFIQACRGSETDGDVGQ      299
Qy    141 -----EIVGGDEIWMWIKDSFOPTITTYDIALHVSIVTBESYAIARHDQKSGCF         187
Db    300 RDGRQGSGSPGCEGCSGAGEDIKV-----RLPTSQDWICAVACLKGTYSINLRTRKGSWF       353
Qy    188 IQTLVDVFTK--RKGHILELTVEVIRMAEAILVDEGKRARKTN-----PEIQSTLRKR      238
```

Db	354	VQDLVSVFSGHSDTHVADKLIVYVNL	IKK----	RESHAGTGEFHRCKEMSEYESTL	CRD 409
QY	239	LYL 241			
Db	410	LYL 412			
RESULT 5					
Q9BUP7					
ID	Q9BUP7	PRELIMINARY;	PRT;	435 AA.	
AC	Q9BUP7				
DT	01-JUN-2001	(TrEMBLrel. 17, Created)			
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)			
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)			
DE	Similar to caspase 2 (Neural cell expressed, developmentally down-regulated 2).				
OS	Human sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skin;				
RA	Strausberg R.;				
RL	Submitted (PEB-2001) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Kalnine N., Chen X., Rolfs A., Halleck A., Hines J., Eisenstein S.,				
RA	Koundinya M., Raphael J., Moreira D., Kelley T., Lahee J., Lin Y.,				
RA	Phelan M., Farmer A.;				
RT	"Cloning of human full-length cDNAs in BD Creator(TM) System Donor				
RT	vector.";				
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC002427; AAH02427.1; -.				
DR	EMBL; BT007240; AAP35904.1; -.				
DR	HSSP; P23465; 1ICE.				
DR	GO; GO:0005622; C:intracellular; IEA.				
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.				
DR	GO; GO:0030693; F:caspase activity; IEA.				
DR	GO; GO:0008233; F:peptidase activity; IEA.				
DR	GO; GO:0006915; P:apoptosis; IEA.				
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR001315; CARD.				
DR	InterPro; IPR002138; ICE_P10.				
DR	InterPro; IPR001309; ICE_P20.				
DR	InterPro; IPR002398; Peptidase_C14.				
DR	Pfam; PF00619; CARD; 1.				
DR	Pfam; PF00656; Peptidase_C14; 1.				
DR	PRINTS; PR00376; TLBENZTIME.				
DR	SMART; SM00134; CARD; 1.				
DR	SMART; SM00115; CASc; 1.				
DR	PROSITE; PS50209; CARD; 1.				
DR	PROSITE; PS01122; CASPASE_CYS; 1.				
DR	PROSITE; PS01121; CASPASE_HIS; 1.				
DR	PROSITE; PS50207; CASPASE_P10; 1.				
DR	PROSITE; PS50208; CASPASE_P20; 1.				
KW	Protease.				
SEQ	SEQUENCE	435 AA;	48869 MW;	10CPA5A1P9369E57 CRC64;	
Query Match		23.3%;	Score 289;	DB 4;	Length 435;
Best Local Similarity		31.1%;	Pred. No. 3.2e-16;		
Matches	74;	Conservative 51;	Mismatches 77;	Indels 36;	Gaps 7
Db	29	REGSEBDLDALEHMFROLPSTFMRDPTAFQFQELKFOQALDSRDPVSCAFVLMNA	88		
QY	202	RSRGDVHSHSTLYTLTKLIGYVHVYICDTTQAEQKLNFAQ-LRAHRTVDSCLYALLS	259		
Db	89	HGRBFLKGEDEGEMVKELEFALNNKXQALIRAKPKVYIIQACRGEQDPG-----	140		
QY	260	HGVGGAIVGVGDKLTLQLEVFQLFDNANCPSLQNKPKMFIQACRGDETRGVDDQDGKN	319		
QY	141	-----ETVGGGEIVVIVINDSQTLITTYDALHIVSTVEYIAYRRDQKSGCTIGLYL	192		

Db 320 HAGSPGCRSDAKB-----KLPKMRUPTRSDMTCGACACKGTAMNTRKSGWYITELA 374
 QY 193 DVFYKR--KHGILLETETVRRAAEIVGGRKRTN-----PEIQSTLRRLYI 241
 Db 375 QVFSEKADMHVADMLVKVALLMD---REGVAPGTEFHRCKEMSEVCSLCHRLYI 428

RESULT 6

093417 PRELIMINARY; PRT; 283 AA.
 ID 093417
 AC 093417
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Caspase-3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20149872; PubMed=10664799;
 RX Johnson A.L., Bridgman J.T.,
 RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
 cells.";
 RL Biol. Reprod. 62:589-598 (2000).
 DR EMBL: AF083029; AAC32602.1; -.
 DR HSSP; P42574; 1PAU.
 DR MEROPS; C14.003; -.
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR SQUENCE 283 AA; 31675 MW; 161242DDEFD4C4F CRC64;

Query Match 23.0%; Score 284.5; DB 13; Length 283;
 Best Local Similarity 30.3%; Pred. NO. 4.6e-16;
 Matches 76; Conservative 47; Mismatches 101; Indels 27; Gaps 7;

QY 7 IEERKYMGSAAALALILCVT-----KAREGSEEDLALHMRQURFESTMKRDP 56
 Db 40 LPDSDYRMDDPELIGVCITINNKNFHRDTGLSSRGTDADAASREVMKLGKYKLANDL 99
 QY 57 TAEQOEELKFKFOQALDSREDPVSCAFVIMAHGREGLFGEDGEMVKLENLFEALNNKN 116
 Db 100 SSADIFKLTKNVSEEDSKSRSSFVC---VLISHGDEGLFYGTGDLPL-ELKVLNLSFRGDK 155
 QY 117 COALRAKPKYIIOACRGEORDPG--ETVGDGLVMWIKSPQTIPIYDALHVSIVGES 174
 Db 156 CRSLAKGKLFYQACRGITLDSGITEDSGPDFTVC-----KRIPEADFLVAYSTAFG 209
 QY 175 YIAYRHDKSGCEIQTIVDVFTK--RKGHILELLETVTRMAAEALV---QESKARKTNP 229
 Db 210 YYSWRNAAGSWMFIQSLCRMLKEHARKLELMQILTVNRRVAVYESGSTQDINAKKQIP 269
 QY 230 EIQSTLRRLYI 240
 Db 270 CIVSMILTKERY 280

RESULT 7
 081780 PRELIMINARY; PRT; 316 AA.
 ID 081780

AC 081780;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Caspase 3.
 OS Geodia cydonium (Sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 OC Astrophorida; Geodiidae; Geodia.
 OX NCBI_TaxID=6047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wiens M., Saenger H., Krasko A., Petrovic S., Mueller W.E.G.;
 RT "Caspase-mediated apoptosis in sponges: cloning and function."
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; A0417903; CADI0676.1; -.
 DR GO; GO:0030693; F:caspase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR Pfam; PF00656; Peptidase_C14.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR SQUENCE 316 AA; 35319 MW; 33A46BCCE6C3F9B7 CRC64;

Query Match 22.6%; Score 279.5; DB 5; Length 316;
 Best Local Similarity 28.2%; Pred. No. 1.4e-15;
 Matches 78; Conservative 54; Mismatches 94; Indels 51; Gaps 9;

QY 9 EEKYMGS--ALALIL-----CVTKARESEEDLALHMRQURFESTMKRDPYAEQ 60
 Db 37 KDAYKMSRPRGMALLIINNFTCGMKERYGTDKDAENLYGLFNWLGMAITRDNLTGXA 96
 QY 61 FOEELKFKFOQALDSREDPVSCAFVIMAHGREGLFGEDGEMVKLENLFEALNNKNQAL 120
 Db 97 MTRFEEDLARDHSAVD---CVVAILTHGISGLYSTDGDLLPVEDLTXYCPDGVNPSL 153
 QY 121 RAKPKYIIOACRGEORDPG--ETVGD-----DEIWMVKDSPOT- 158
 Db 154 IKGPKYFVYQACGKGFYVSESESTDGESVYNKETANEMKQPPKIVKALDAPETD 213
 QY 159 -----IPTYDALHVSIVTVEGYIAYRHDKSGCEIQTIVVF--TKRGHILELLE 208
 Db 214 GCGYSREALPTEADFVLAVATVPGYVSWRNSWFIKAFVDVTRMDLAKSEHMDILTE 273
 QY 209 VTRRMAAEIVGGRKRTNPEIQ---STLRKRLYI 242
 Db 274 VNRKVA-----YDFOSRGRKQIPAPVTMLTRXLTER 305

RESULT 8

0816Y2 PRELIMINARY; PRT; 426 AA.
 ID 0816Y2
 AC 0816Y2
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Caspase-3.
 GN Geodia cydonium (sponge).
 OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 OC Astrophorida; Geodiidae; Geodia.
 OX NCBI_TaxID=6047;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Eukaryota;
 RA Wiens M., Saenger H., Krasko A., Petrovic S., Mueller W.E.G.;
 RT "Caspase-mediated apoptosis in sponges: cloning and function."
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.

Query	Match	Best Local Similarity	22.6%	Score 279.5	DB 5	Length 426
Matches	78	Conservative	54	Mismatches	94	Indels 51; Gaps 9
Qy	9	EEKDMSG--AALAIL-----CYTKARSGEEDLDALENHFRQRLRFSTSTKRPDTAQ 60				
Db	147	KDAVKMSRPRGMALINNRFCTGCKMRVGDCKAENLYGIFNNLGMATIRKDLTGTA 206				
Qy	61	FQEELEKQQAIDSIEDPVSCAFVYLMAGREGFLKGEDEGWKXENLFEALNKKCOAL 120				
Db	207	MTRFEFDLARDHSHAYD---CVVAALIHGISGRILXSTDGDLIPEDLTIKYDGVNRRBL 263				
Qy	121	RAKRPVYLIOACRGQRDPG---ETVGG-----DEIVWIKDSPOT 158				
Db	264	IGRKRVFVVOACRGKFPDYGVSESTDEGSEVNKETANEMWEKQFDKVEKALDADET 223				
Qy	159	-----LPTYTDAIHVYSTVEGYIAYRHDKGSCFIQTLVDV--TYRKCHILLELLE 208				
Db	324	GGGYSREALPLEADFVLAYATVPVGYSMRNSRSGWFIKAFVDTRDLASKHFMDILTE 383				
Qy	209	VTREMAEAELVQEGKARKTNPQIO---ETPKRYLQ 242				
Db	384	VNRKVA-----YDFSGRGRNKKQIPAPVTMLTKLYFR 415				

RESULT 9

Q8MUC3 PRELIMINARY; PRT; 277 AA.

AC Q8MUC3; TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, last annotation update)

DE Cysteine protease CPP32.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_Taxid=9986;

RN

RP SEQUENCE FROM N.A.

RA Wang H., Keiser J.A.,

RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF506008; AAM47195.1; -

DR GO; GO:0030693; F:casepase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR002138; ICE_p10.

DR InterPro; IPR002398; Peptidase C14.

DR Pfam; PF00656; Peptidase C14; I.

DR PRINTS; PR00376; ILBCEZYME.

DR SMART; SM00115; CASc_1.

DR PROSITE; PS01122; CASPASE_CYS_1.

DR PROSITE; PS01121; CASPASE_HIS_1.

DR PROSITE; PS0207; CASPASE_P10; 1.

DR PROSITE; PS0208; CASPASE_P20; 1.

SO SEQUENCE 426 AA; 48024 MW; 71B5EEC82EED0C1 CRC64;

Query Match	22.2%	Score 275.5;	DB 6;	Length 277;
Best Local Similarity	33.3%	Pred. No. 2.6e-15;		
Matches	84;	Conservative 39;	Mismatches 105;	Indels 27; Gaps 8;
Qy	9	EEKYDMSGAALALILCVT-----KAREGSEEDLDALEHFRQLRFESTMKRDP	58	
Db	34	DNSIKMIMYEMGLCIITINNNKFNKMTGSSSGTDVNAANGELFMILKTYVRANKDL	93	
Qy	59	EQFOEELKEKQOALDSREDPYSCAFVYIMAHGREBFLKGEDGEVKKLENIFEALNNKCQ	118	
Db	94	EELMELWYNVNSKEDHSKRSPIC---VILSHGDEGVIYGTNGP-IEKKLTSPFRGDYCR	149	
Qy	119	ALRAKPKVYIIQARAGQCRDPG-ETVGDELEVMIYKSPQIIPTTDAIHYSTVEG	177	
Db	150	SLTKRKPLFTIIQAGRGTELDGSLTDSGVDMAC---QKTIPEADPLVYSTAPGY	205	
Qy	178	YRHQKQSCFIQTVDFETKRKHILE---LLTEVTRMA---EAEIVQEGKARKTPE	230	
Db	206	WRNEBEGSWFIQSLC-AMLEKAYAKLEFMHILTVNNKVAKEFEESYSLDAIFHAKKQ	264	
Qy	231	IQSTLRKRLY 240		
Db	265	IVSMULTKELY 274		
RESULT 10				
Q8MJU1				
ID	Q8MJU1	PRELIMINARY;	PRU;	277 AA.
AC	O8MJU1			
DT	01-OCT-2002	(TREMBLrel. 22. Created)		
DT	01-OCT-2002	(TREMBLrel. 22. Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25. Last annotation update)		
DE	Caspase3.			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Carnivora; Fissipedia; Felidae; Felis.			
OX	NCBI_TaxID=9685;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yamazaki J., Sano R., Hasegawa A.;			
RT	"Felis catus mRNA for caspase3, complete cds."			
RL	Submitted (Aug-2002) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AB090246; BAC10589.1; -			
DR	GO; GO:0030693; F:caspase activity; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR002138; ICE P10.			
DR	InterPro; IPR002398; Peptidase_C14.			
DR	Pfam; PF00656; Peptidase_C14; I.			
DR	PRINTS; PR00376; ILBCENZME.			
DR	SMART; SMO0115; CASC; 1.			
DR	PROSITE; PS01122; CASPASE_CYS; 1.			
DR	PROSITE; PS01121; CASPASE_HIS; 1.			
DR	PROSITE; PS0207; CASPASE_P10; 1.			
DR	PROSITE; PS50208; CASPASE_P20; 1.			
SO	SEQUENCE 277 AA; 31465 MW; 8749679C30ABA6F6 CRC64;			
Query Match	22.2%	Score 275.5;	DB 6;	Length 277;
Best Local Similarity	33.3%	Pred. No. 2.6e-15;		
Matches	84;	Conservative 35;	Mismatches 102;	Indels 31; Gaps 10;
Qy	9	EEKYDMSGAALALILCVT-----AREGSEEDLDALEHFRQLRFESTMKRDP	58	
Db	34	DNSYKMDPEKGLCIITINNNKFNHSTGWSGTDVDAANRLEPTTNKYEVRRNKD	93	
Qy	59	EQFOEELKEKQOALDSREDPYSCAFVYIMAHGREBFLKGEDGEVKKLENIFEALNNKCQ	118	
Db	94	EELMELWYNVNSKEDHSKRSPIC---VILSHGDEGVIYGTNGP-IEKKLTSPFRGDYCR	149	
Qy	119	ALRAKPKVYIIQARAGQCRDPG-ETVGDELEVMIYKSPQIIPTTDAIHYSTVEG	177	
Db	150	SLTKRKPLFTIIQAGRGTELDGSLTDSGVDMAC---QKTIPEADPLVYSTAPGY	205	
Qy	178	YRHQKQSCFIQTVDFETKRKHILE---LLTEVTRMA---EAEIVQEGKARKTPE	230	
Db	206	WRNEBEGSWFIQSLC-AMLEKAYAKLEFMHILTVNNKVAKEFEESYSLDAIFHAKKQ	264	
Qy	231	IQSTLRKRLY 240		
Db	265	IVSMULTKELY 274		

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Db      94  EQIYALDVSAREHSHKRSFFIC--VLLSHGEGIIYGTNGP-VDLKKLTGPFPGDYCR 149
QY      119  ALRKPXYITIOACRGEGRDPG-ETVGG--DEIMVNIKDSQOTIPTYDALHVSIVTEGY 175
Db      150  SLTGKPKFIIOACRGELDLGILTDSTEDDLC-----OKIPEVADFIYASTAGY 203
QY      176  IAYHHDGKSGCFIOTLVDFTRKHILE--LITEVTRMA-EAEIVQEGKA--RKTN 228
Db      204  YSMNNSKDGSWFIQSLCSML-RLVAHELEFHHILTRVNRKATATFESISLDSAFHGKQI 262
QY      229  PETOSTLRKRY 240
Db      263  PCIVSMLTKEYI 274

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RESULT 11

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ID      095ND5      PRELIMINARY;      PRT;      277 AA.
AC      095ND5;
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
OS      Caspase-3.
OC      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX      NCBI_TaxId=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21334413; PubMed=11440638;
RA      Muneta Y., Shimojima Y., Mori Y.;
RT      "Porcine caspase-3: cloning and its activity during apoptosis of
RL      porcine PK15 cells induced by porcine Fas-ligand.";
EMBL: AB029345; BAB55544.1; -.
DR      MEROPS; C14.003; -.
DR      GO; GO:0030693; F:caspase activity; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR002138; ICE p10.
DR      InterPro; IPR001309; ICE p20.
DR      InterPro; IPR002398; Peptidase_C14.
DR      Pfam; PF00656; Peptidase_C14; 1.
DR      PRINTS; PR00376; IL1BCENZYM.
DR      SMART; SM00115; CASC; 1.
DR      PROSITE; PS01122; CASPASE_CYS; 1.
DR      PROSITE; PS01121; CASPASE_HIS; 1.
DR      PROSITE; PS50207; CASPASE_P10; 1.
DR      PROSITE; PS50208; CASPASE_P20; 1.
SQ      SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

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Query Match 22.2%; Score 274.5; DB 6; Length 277;

Best Local Similarity 37.3%; Pred. No. 3, 1e-15;

Matches 82; Conservative 27; Mismatches 94; Indels 17; Gaps 8;

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QY      29  RSGSEEDLALHMFQRLRSTMKRDPPTAEQOELEKFOQALDSREDPVSCAFVYMA 88
Db      64  RSGTDVDAANILRFTFNMLKYEVRKNDLTREELILMHVSFKEDHGRSSFFIC--VLLS 120
QY      89  HGESEGLKGGEDGMVLENLFEALNNKCOALRAKRYVITIOACRGEGRDPG-ETVGGDE 147
Db      121  HGESEGLKGGEDGMVLENLFEALNNKCOALRAKRYVITIOACRGEGRDPG-ETVGGDE 179
QY      148  IYVWIKDSQOTIPTYDALHVSIVTEGYTAYRHQDQSGCFIOTLVDFTRKHILE-- 205
Db      180  DDVAC-----OKIPEVADFIYASTAGYSWMNSKDGSWFIQSLCAL-KQYVHKLLEMH 234
QY      206  -LITEVTRMA-EAEIVQEGK--ARKTNPEIQTSLRKRY 240
Db      235  ILTRVNRKATATFESISLDSAFHGKQI 274

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RESULT 12

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Q919L7
ID      0919L7      PRELIMINARY;      PRT;      383 AA.
AC      0919L7;
DT      01-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
OS      Caspase.
GN      CASPA OR CASPY.
OC      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxId=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20373792; PubMed=10917738;
RA      Inohara N., Nunez G.;
RT      "Genes with homology to mammalian apoptosis regulators identified in
RT      zebrafish.";
RL      Cell Death Differ. 7:509-510(2000).
DR      EMBL; AF233434; AAC66964.1; -.
DR      HSP; P29466; IICE.
DR      ZFIN; ZDB-GENE-000616-3; caspa.
DR      GO; GO:0030693; F:caspase activity; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR002138; ICE p10.
DR      InterPro; IPR001309; ICE p20.
DR      InterPro; IPR004020; PAAD-DAPIN dom.
DR      InterPro; IPR002398; Peptidase_C14.
DR      Pfam; PF02758; PAAD-DAPIN; 1.
DR      Pfam; PF00656; Peptidase_C14; 1.
DR      PRINTS; PR00376; IL1BCENZYM.
DR      SMART; SM00115; CASC; 1.
DR      PROSITE; PS01122; CASPASE_CYS; 1.
DR      PROSITE; PS01121; CASPASE_HIS; 1.
DR      PROSITE; PS50207; CASPASE_P10; 1.
DR      PROSITE; PS50208; CASPASE_P20; 1.
SQ      SEQUENCE 383 AA; 43966 MW; 21890871309774C3 CRC64;

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Query Match 22.2%; Score 274.5; DB 13; Length 383;

Best Local Similarity 30.0%; Pred. No. 4, 7e-15;

Matches 69; Conservative 49; Mismatches 83; Indels 29; Gaps 6;

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QY      29  RSGSEEDLALHMFQRLRSTMKRDPPTAEQOELEKFOQALDSREDPVSCAFVYMA 88
Db      162  RSGSEKDEENMERKLAKELDYQVVKRPNLSAKENDAIRDPAQREHKKYS--DSAFVIMS 219
QY      89  HGESEGLKGGEDGMVLENLFEALNNKCOALRAKRYVITIOACRGEGRDPG-ETVGGDE 137
Db      220  HGRKDAIMGVHNHRTNPNPDSFVVDVNYRLNSENCPLADKFKVILIOACRGEGRGMV 279
QY      138  ---DGEIVGDEIYVNIKDSQOTIPTYDALHVSIVTEGYTAYRHQDQSGCFIOTLV 193
Db      280  ASDGEDEPLEIEDDDFVHKK-----DFISLMSCPDPTSKSYHVQGTGYVQTLVD 331
QY      194  VETK--RKHHILELITEVTRMAEALVQEGARKTNPEIQTSLRKRY 241
Db      332  VETKCAHEHIELEFRKVLRRFEHFNMT--GNFKQACRDRATLPLFYI 379

```

RESULT 13

```

ID      08CHV5      PRELIMINARY;      PRT;      313 AA.
AC      08CHV5;
DT      01-MAR-2003 (TREMBlrel. 23, Created)
DT      01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE      01-OCT-2003 (TREMBlrel. 25, Last annotation update)
OS      Caspase 3, apoptosis related cysteine protease (Fragment).
GN      CASP3.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:39:36 ; Search time 43.438 Seconds
(without alignments)
949.674 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146

Perfect score: 752
Sequence: 1 MSNPRSLREKXDMGALA.....YIIQACRGSRDPTGVGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	DB ID	Description
1	747	99.3	230 3	AAY93215 Amino aci
2	747	99.3	242 3	AAY93214 Amino aci
3	747	99.3	242 5	AAG77980 Full-leng
4	702	93.4	224 5	AAG77984 Full-leng
5	679	90.3	229 3	AAY68865 Amino aci
6	586	77.9	257 3	AAY68864 Amino aci
7	586	77.9	281 3	AAY93592 Mouse cas
8	578	76.9	214 3	AAY93216 Amino aci
9	300.5	40.0	234 5	AAY93213 Human asp
10	300.5	40.0	398 5	AAY72882 Human asp
11	210	27.9	435 2	AAR66771 Human int
12	210	27.9	435 2	AAR66771 Human int
13	210	27.9	435 2	AAR98462 Human ice
14	210	27.9	435 2	AAR98462 Human ice
15	210	27.9	435 2	AAR90703 Interleuk
16	210	27.9	435 2	AAR90703 Interleuk
17	210	27.9	435 2	AAR90703 Interleuk
18	210	27.9	435 2	AAR90703 Interleuk
19	210	27.9	435 2	AAR90703 Interleuk
20	210	27.9	435 2	AAR90703 Interleuk
21	210	27.9	435 2	AAR90703 Interleuk
22	210	27.9	435 2	AAR90703 Interleuk
23	210	27.9	435 2	AAR90703 Interleuk
24	210	27.9	435 2	AAR90703 Interleuk
25	205	27.3	452 7	AAB79812 Rat caspa

ALIGNMENTS

26	205	27.3	452 7	ADE63000 Rat Prote
27	197	26.2	312 2	AAR66772 Human int
28	197	26.2	312 2	AAR98463 Human ice
29	197	26.2	312 3	AAB14258 Human ich
30	197	26.2	312 4	AAE00616 Human cas
31	197	26.2	312 5	AAU96868 Human cas
32	197	26.2	457 7	AAW25766 Human pro
33	196	26.1	435 3	AAB14262 Mutant hu
34	190.5	25.3	250 4	AAB98653 Caspase-1
35	189	25.1	404 2	AAV01315 Canine in
36	189	25.1	404 3	AAW82559 Canine in
37	189	25.1	404 3	AAW82561 Canine in
38	187.5	24.9	256 4	AAW59580 Human cas
39	187.5	24.9	311 2	AAW00994 Interleuk
40	187.5	24.9	323 2	AAW00988 Human int
41	187.5	24.9	339 2	AAW00989 Human int
42	187.5	24.9	383 2	AAW00993 Interleuk
43	187.5	24.9	383 4	AAE00615 Human cas
44	187.5	24.9	394 2	AAR33779 ICE. 3/20
45	187.5	24.9	404 2	AAR15745 Interleuk

RESULT 1
AAY93215
ID AAY93215 standard; protein; 230 AA.

AC AAY93215;

DT 04-SRP-2000 (first entry)

DE Amino acid sequence of a human caspase-14 splice variant.

KM Caspase-14; cell death specific protease; apoptosis stimulator;
KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

OS Homo sapiens.

FT Key Location/Qualifiers
FT Active-site 130..134

PN W0200028047-A1.

PD 18-MAY-2000.

PF 29-OCT-1999; 99WO-US025523.

PR 06-NOV-1998; 98US-00187789.

PA (UYJE-) UNIV JEFFERSON THOMAS.

PI Alnemri ES, Fernandez-Alnemri T;

DR WPI, 2000-376558/32.

DR N-PSDB; AAA15165.

XX Novel nucleic acids encoding cell death specific protease termed caspase-14 useful for treating cancers by stimulating apoptosis.

PT Claim 41; Fig 8; 78pp; English.

PS The present sequence represents a human caspase-14 splice variant. The polypeptide is a cell death specific protease, and is an apoptosis stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase-14 antibodies are useful for treating or reducing the severity of pathological conditions associated with increased or decreased levels of apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative diseases and ischemic injury are treated by administering anti-caspase-14 antibodies. The antibody is useful for determining the presence of the level of caspase-14 in tissue sample and also for the isolation of caspase-14 with apoptotic activity or in screening assay to identify an

CC agent that inhibits heterodimer or heterotetramer formation and
CC therefore, apoptosis
XX
SQ Sequence 230 AA;

Query Match 99.3%; Score 747; DB 3; Length 230;
Best Local Similarity 99.3%; Pred. No. 7.4e-76;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDLEHMFRLRRESTMKRDPPTAEQ 60
Db 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDLEHMFRLRRESTMKRDPPTAEQ 60
QY 61 FOEIEKFKQAIDSRDPVSCAFVVLMAHGREGFLKGDGEMVKLENFEALNNKNCAL 120
Db 61 FOEIEKFKQAIDSRDPVSCAFVVLMAHGREGFLKGDGEMVKLENFEALNNKNCAL 120
QY 121 RAKPKVYIIQACRGEQRDPGETVGSD 146
Db 121 RAKPKVYIIQACRGEQRDPGETVGSD 146

RESULT 2

AAV93214
ID AAV93214 standard; protein; 242 AA.

XX
AC AAV93214;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of a human caspase-14.

XX
KM Caspase-14; cell death specific protease; apoptosis stimulator;
KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT Region 1..146

FT Active-site /note= "large subunit" 130..134

FT Cleavage-site 146..147

FT Region 147..242

FT /note= "small subunit"

PN WO200028047-A1.

PD 18-MAY-2000.

PF 29-OCT-1999; 99WO-US025523.

PR 06-NOV-1998; 98US-00187789.

PA (UYUE-) UNIV JEFFERSON THOMAS.

PI Alnemri ES, Fernandez-Alnemri T;

XX
XX WPI; 2000-376558/32.

DR N-PSDB; AAA15164.

PT Novel nucleic acids encoding cell death specific protease termed caspase-14
PT 14 useful for treating cancers by stimulating apoptosis.

PS Claim 13; Fig 7; 78pp; English.

XX
XX The present sequence represents a human caspase-14 polypeptide. The
CC polypeptide is a cell death specific protease, and is an apoptosis
CC stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
CC -14 antibodies are useful for treating or reducing the severity of
CC pathological conditions associated with increased or decreased levels of
CC apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
CC diseases and ischemic injury are treated by administering anti-caspase-14
CC antibodies. The antibody is useful for determining the presence or the

CC level of caspase-14 in tissue sample and also for the isolation of
CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotetramer formation and
CC therefore, apoptosis
XX
SQ Sequence 242 AA;

Query Match 99.3%; Score 747; DB 3; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.9e-76;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDLEHMFRLRRESTMKRDPPTAEQ 60
Db 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDLEHMFRLRRESTMKRDPPTAEQ 60
QY 61 FOEIEKFKQAIDSRDPVSCAFVVLMAHGREGFLKGDGEMVKLENFEALNNKNCAL 120
Db 61 FOEIEKFKQAIDSRDPVSCAFVVLMAHGREGFLKGDGEMVKLENFEALNNKNCAL 120
QY 121 RAKPKVYIIQACRGEQRDPGETVGSD 146
Db 121 RAKPKVYIIQACRGEQRDPGETVGSD 146

RESULT 3

AAG77980
ID AAG77980 standard; protein; 242 AA.

XX
AC AAG77980;

DT 05-APR-2002 (first entry)

DE Full-length human caspase-14.

XX
KM Human; caspase-14; anti-apoptotic; apoptosis.

XX
OS Homo sapiens.

PN WO200181595-A2.

PD 01-NOV-2001.

PF 27-APR-2001; 2001WO-US013831.

PR 27-APR-2000; 2000US-0199962P.

PA (KNOL) KNOLL GMBH.

PI Mankovich JA;

XX
XX WPI; 2002-041410/05.

DR N-PSDB; AAK98248.

PT Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.

PS Claim 20; Fig 1; 58pp; English.

XX
XX The sequence represents the novel full-length human caspase-14 protein,
CC referred to as "Caspase-14 NEW" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino
CC acid sequence with MSNPRSLSE, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in

CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein
XX
SQ Sequence 242 AA;

Query Match 99.3%; Score 747; DB 5; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.9e-76;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEKPYDMSGALALILCYTKAREGSEEDLDALHMFRLRFESTMKRDPTAQ 60
DB 1 MSNPRSLSEKPYDMSGALALILCYTKAREGSEEDLDALHMFRLRFESTMKRDPTAQ 60
QY 61 FQELERKFOALIDSRDPVSCAFVVLMAHGREGFLKGEDEGVKLENTFEALNNKCOAL 120
DB 61 FQELERKFOALIDSRDPVSCAFVVLMAHGREGFLKGEDEGVKLENTFEALNNKCOAL 120
QY 121 RAKPKYVITIQCRCGEQRPGETVGGD 146
DB 121 RAKPKYVITIQCRCGEQRPGETVGGD 146

RESULT 4
AAG77984
ID AAG77984 standard; protein; 242 AA.
XX
AC AAG77984;
XX
DT 05-APR-2002 (first entry)
XX
DE Full-length human caspase-14 old.
XX
KM Human; caspase-14; anti-apoptotic; apoptosis.
XX
OS Homo sapiens.
XX
PN WC200181595-A2.
XX
PD 01-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US013831.
XX
PR 27-APR-2000; 2000US-0199962P.
XX
PA (KNOL) KNOLL GMBH.
XX
PI Mankovich JA;
XX
DR WPI; 2002-041410/05.
XX
PT Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.
XX
XX

PS Example; Fig 1; 58pp; English.

CC The sequence represents the full-length human caspase-14 protein,
CC referred to as "Caspase-14 OLD" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino
CC acid sequence with MSNPRSLSE, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14

CC protein
XX
SQ Sequence 242 AA;

Query Match 93.4%; Score 702; DB 5; Length 242;
Best Local Similarity 99.3%; Pred. No. 9.6e-71;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 EKYDMSGALALILCYTKAREGSEEDLDALHMFRLRFESTMKRDPTAQEQFQELERKQ 69
DB 10 EKYDMSGALALILCYTKAREGSEEDLDALHMFRLRFESTMKRDPTAQEQFQELERKQ 69
QY 70 QALIDSRDPVSCAFVVLMAHGREGFLKGEDEGVKLENTFEALNNKCOALRAKPKYVITI 129
DB 70 QALIDSRDPVSCAFVVLMAHGREGFLKGEDEGVKLENTFEALNNKCOALRAKPKYVITI 129
QY 130 QACRCGEQRPGETVGGD 146
DB 130 QACRCGEQRPGETVGGD 146

RESULT 5
AA68865
ID AA68865 standard; protein; 229 AA.
XX
AC AA68865;
XX
DT 16-MAY-2000 (first entry)
XX
DE Amino acid sequence of a human caspase-like polypeptide.
XX
KM Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
KM Keratinisation; wound healing.
XX
OS Homo sapiens.
XX
PN WC200004169-A1.
XX
PD 27-JAN-2000.
XX
PF 12-JUL-1999; 99WO-EP004939.
XX
PR 17-JUL-1998; 98EP-00202422.
XX
PA (VLAAS-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Van De Craen M, Declercq W, Vandenaabeele P, Piers W;
XX
DR WPI; 2000-182433/16.
XX
DR N-PSDB; AA260684.
XX
PT New murine and human caspase homologues useful for treating skin related
PT disorders.
XX
XX

PS Claim 2; Page 53-54; 68pp; English.

CC The present sequence represents a human caspase-like polypeptide. The
CC specification also describes a murine caspase-like polypeptide. Caspases
CC are cysteine/aspartate-specific proteinases which play a central role in
CC apoptosis. The polypeptides of the invention are related to human and
CC murine caspase-2 and human caspase-9, and possess all of the typical
CC amino acids involved in catalysis, including the QACRG box, and contain
CC no or only a very short prodomain. mRNA expression of the homologues of
CC the invention is predominant in the skin. The caspase-like polypeptides
CC are useful for treating human or animal diseases, such as skin diseases.
CC They are also useful for screening for compounds that modulate its
CC activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
CC polypeptides and polynucleotides are useful for modulating
CC keratinisation, for diagnosing and treating inappropriate wound healing

Query Match 90.3%; Score 679; DB 3; Length 229;
SQ Sequence 229 AA;

```
I MSNPRSLSEEEKYDMSCAALAILCTKAREGSEEJLDLAEHMRQÖLPFESTWKRDPTEAQ 60
```

This invention describes a novel murine caspase-14 which has protease activity. The caspase-14 polypeptide is useful for identifying (ant)agonists of the polypeptide, where enzyme activity is measured with a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated caspase-14 is useful for identifying inhibitors or enhancers of caspase-14 activity. The compounds identified by both methods form pharmaceutical compositions for treating apoptotic-related diseases, including autoimmune disease, cancer, acquired immunodeficiency syndrome (AIDS), neurodegenerative diseases and ischemic injury. The anti-caspase-14 antibody is useful for measuring the level of caspase-14 in a tissue sample. An antibody that binds to a caspase-14 polypeptide is useful for isolating the polypeptide, and an antibody that binds to the large or small subunit the polypeptide is useful for identifying samples with caspase-14 processing activity. An antibody that binds to caspase-14 heterodimer or heterotrimer is useful for isolating caspase-14 with apoptotic activity or in a screening assay to identify (ant)agonists. The antibodies form kits for such purposes. The anti-caspase-14 antibody is also useful for preparing anti-idiotypic antibodies, which mimic a caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore, the antibody is useful as a competitor of caspase-14 in reducing the level of caspase-14 activity, which reduces the level of apoptotic activity. Oligonucleotides made from the polynucleotides are useful as polymerase chain reaction (PCR) primers or probes to screen genomic or cDNA libraries for similar caspase-14 encoding polynucleotides, or for

CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotrimer formation and
CC therefore, apoptosis

XX Sequence 214 AA;

Query Match 76.9%; Score 578; DB 3; Length 214;
Best Local Similarity 80.1%; Pred. No. 8.5e-57;
Matches 117; Conservative 0; Mismatches 1; Indels 28; Gaps 1;

QY 1 MSNRSLSLEEKYKMSGALALILCYTKARSGSEEDLDLHEMFRLQRPSTMRKDPPTAAEQ 60
DB 1 MSNRSLSLEEKYKMSGALALILCYTKARSGSE----- 34

QY 61 FOEELERKQALIDREDPVSCAFVYLMAHGREGFLKGEDEWVKLENLEFALNNKCOAL 120
DB 35 --EELEKFGQALIDREDPVSCAFVYLMAHGREGFLKGEDEWVKLENLEFALNNKCOAL 92

QY 121 RAKPKVYIIQACRGQRDPGRTVGAD 146
DB 93 RAKPKVYIIQACRGQRDPGRTVGAD 118

RESULT 10

AAU72882 standard; protein; 234 AA.

AAU72882;

26-FEB-2002 (first entry)

Human aspartyl protease partial protein sequence #7.

XX Human; protease; PCR primer; cytosolic; immunomodulator; cardiac;
XX vasotropic; antidiarrheal; analgesic; endocrine; neurotropic; tranquiliser;
XX hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;
XX anorectic; antiinflammatory; aspartyl protease; cysteine protease;
XX metalloprotease; serine protease; cancer; haematopoietic; breast;
XX lung; prostate; cervical; brain; ovarian; bladder; kidney; pain;
XX immune-related disease; cardiovascular disease; neuronal disease;
XX migraine; sexual dysfunction; mood disorder; attention disorder;
XX cognition disorder; hypotension; hypertension; psychotic disorder;
XX dyskinnesia; metabolic disorder; inflammatory disorder.

XX Homo sapiens.

MO200183782-A2.

08-NOV-2001.

04-MAY-2001; 2001MO-US014431.

04-MAY-2000; 2000US-0201879P.

(SUGEN-) SUGEN INC.

PJowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;

Payne V;

WPI; 2002-041502/05.

N-FSDB; AAS97165.

Novel protease polypeptide useful for screening for substances that may

Claim 28; Fig 2A; 232PP; English.

XX The invention relates to an isolated, enriched, or purified protease
XX polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to
XX screen for substances (S) that may modulate its activity. Administering S
XX (which modulates protease activity in vitro) may be used to treat a
XX disease or disorder selected from cancers (e.g., of tissues, of blood or

CC haematopoietic origin, of the breast, colon, lung, prostate, cervical,
CC brain, ovarian, bladder or kidney), immune-related diseases and
CC disorders, cardiovascular disease, brain or neuronal-associated diseases
CC (e.g., central or peripheral nervous system diseases, migraine, pain,
CC sexual dysfunction, mood disorders, attention disorders, cognition
CC disorders, hypotension, hypertension, psychotic disorders, neurological
CC disorders and dyskinnesia), metabolic disorders and inflammatory
CC disorders. (I) may also be useful as a diagnostic tool for a disease or
CC disorder such as those above. AAU72876-AAU72910 represent human protease
CC amino acid sequences of the invention

XX Sequence 234 AA;

Query Match 40.0%; Score 300.5; DB 5; Length 234;
Best Local Similarity 46.6%; Pred. No. 2.2e-25;
Matches 61; Conservative 28; Mismatches 39; Indels 3; Gaps 2;

QY 11 KYDMSGALALILCYTKARSGSEEDLDLHEMFRLQRPSTMRKDPPTAORFELERKQ 70
DB 1 QYDLSKRALILAVIOGRGQCHDVVALGGLCALGFTVTRIDPTAORFELERKQ 60

QY 71 AIDSREDPVSCAFVYLMAH-GREGFLKGEDEWVKLENLEFALNNKCOALRAKPKVYII 129
DB 61 QLDTCRGVPVSCAFVYLMAHGGRGQLIGADQGVQVPEALMQELS--RCQVIGRPKFEL 118

QY 130 QACRGQRDPG 140
DB 119 QACRGQRDPG 129

RESULT 11

ABG76499 standard; protein; 398 AA.

ABG76499;

05-NOV-2002 (first entry)

DNA encoding protein modification and maintenance molecule #3.

XX Protein modification and maintenance molecule; gastrointestinal disorder;
XX dysphagia; esophageal spasm; gastritis; anorexia; nausea; hypertension;
XX cardiovascular disorder; atherosclerosis; vasculitis; aneurysm; allergy;
XX ischaemic heart disease; autoimmune disorder; inflammatory disorder;
XX acquired immunodeficiency syndrome; AIDS; ankylosing spondylitis; cancer;
XX anaemia; amyloidosis; cell proliferative; arteriosclerotic bursts;
XX cirrhosis; developmental disorder; renal tubular acidosis; anaemia;
XX bone resorption; epilepsy; epithelial disorder; keratosis pilaris;
XX allergic contact dermatitis; insect bite; keloid; dermatofibroma; eczema;
XX neurological disorder; stroke; cerebral neoplasm; Alzheimer's disease;
XX Huntington's disease; dementia; reproductive disorder; infertility;
XX endometriosis; gynecomastia; ectopic pregnancy; gene therapy.

XX Homo sapiens.

WO200260942-A2.

08-AUG-2002.

30-JAN-2002; 2002MO-US002813.

31-JAN-2001; 2001US-0265705P.

05-FEB-2001; 2001US-0266762P.

16-FEB-2001; 2001US-0269581P.

23-FEB-2001; 2001US-0271198P.

01-MAR-2001; 2001US-0272813P.

13-MAR-2001; 2001US-0275586P.

23-MAR-2001; 2001US-0278505P.

30-MAR-2001; 2001US-0280539P.

(INCY-) INCYTE GENOMICS INC.

Warren BA, Honchell CD, Lu Y, Walia NK, Burford N, Delegeane AM;

P	Gandhi AR, Baughn MR, Griffin JA, Gietzen KT, Lu DAM, Ison CH,
P	Ramkumar J, Tang TY, Lai PG, Borowski M., Dugan BM, Hafalia AJA;
P	Arvivu C, Thangavealu K, Yao MG, Elliott VS, Ding L, Yue H, Lee S;
X	Swarnakar A, Tran UK, Xu Y;
D	WP1; 2002-608499/65.
D	N-FSDB; ABS56370.
X	
P	New protein modification and maintenance molecules useful for treating or preventing gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, neurological and reproductive disorders.
P	
P	Claim 1; Page 133-134; 172pp; English.
X	
C	The invention describes an isolated human polypeptide (I), a naturally occurring amino acid sequence at least 90 % identical to the protein, or a biologically active fragment or an immunogenic fragment of the protein.
C	The protein modification and maintenance molecules are useful in the diagnosis, treatment, and prevention of gastrointestinal (e.g. dysphagia, esophageal spasm, gastritis, anorexia or nausea), cardiovascular (e.g. atherosclerosis, hypertension, vasculitis, aneurysms, or ischemic heart disease), autoimmune/inflammatory (e.g. acquired immunodeficiency syndrome (AIDS), allergies, arkylosing spondylitis, anaemia or amyloidosis), cell proliferative (e.g. cancers, arteriosclerotic, burstils, or cirrhosis), developmental (e.g. renal tubular acidosis, CC anaemias, bone resorption, or epilepsy), epithelial (e.g. allergic contact dermatitis, keratosis pilaris, insect bites, keloid, dermatofibroma or eczema), neurological (e.g. stroke, cerebral neoplasms, Alzheimer's disease, Huntington's disease or dementia), and reproductive disorders (e.g. infertility, endometriosis, gynecomastia or ectopic pregnancy).
C	These may also be used in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences or protein modification and maintenance molecules. Polynucleotides are useful in somatic and germline gene therapy. This is the amino acid sequence of a protein modification and maintenance molecule described in the invention
X	
SQ	Sequence 398 AA:
Query Match	40.0%; Score 300.5; DB 5; Length 398;
Best Local Similarity	46.6%; Pred. No. 4.5e-25;
Matches 61; Conservative 28; Mismatches 39; Indels 3; Gaps 2	
Yq	11 KYDSGALAILCVTKARSGSEEDLDIAIHMFROLRFEFTSKRDPDAFOPEBELKPOO 70 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: 165 QYDLSKAPAAALLAVIOGRPPAQHVEALGGICWMLGFETVTRPTAOAFOBELLOFRE 224
Oy	71 AIDSREDPVSACFVLIMAH-GREGFLKEKDGEWKLEN:FELNNNGCALAKPKVYLII 129 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : Db 225 QLDTGRGPVSCVALVMHGPRGOILGDAGOEVPDEALMOELS-RCYVOLGRPIFYLL 282
Oy	130 OACRGEOBDPG 140 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: : Db 283 OACRGANRDAG 293
RESULT 12	
AAR66771	ID AAR66771 standard; protein; 435 AA.
XX AC	AAR66771;
XX XX	
DT DT	25-MAR-2003 (revised)
DT DT	13-SEP-1995 (first entry)
XX DE	Human interleukin-1 beta convering enzyme ced 3 homolog Ich-1(L) .
XX KM	Human inter-leukin-1 beta converting enzyme ced 3 homolog; Ich-1(L); oncogene hol-2; programmed cell death; cancer treatment.
KM XX	Homo sapiens.
OS Key	Location/Qualifiers
FH XX	

FT	Active-site	301..305
XX		
PN	M09500160-AL	
XX		
PD	05-JAN-1995.	
XX		
PF	10-JUN-1994;	94MO-US006630.
XX		
PR	24-JUN-1993;	93US-00080850.
XX		
PA	(GEHO) GEN HOSPITAL CORP.	
XX		
PI	Yuan J, Miura M;	
XX		
DR	WPI; 1995-051742/07.	
XX		
DR	N-PDSB; AAQ79971.	
XX		
PT	or preventing programmed cell death in vertebrate cells - by inhibiting	
PT	the activity of interleukin-1 beta converting enzyme.	
XX		
PS	Example 5; Fig 12A; 116pp; English.	
XX		
CC	AAQ79971 encodes AAR66771 human interleukin-1 beta converting enzyme ced	
CC	3 homolog Ich-1(I), increasing Ich-1(I)'s enzymatic activity can promote	
CC	the programmed cell death of cancer cells (pref. those overexpressing the	
CC	bcl-2 oncogene), this can be used as the basis of a new cancer treatment.	
CC	Alternatively by reducing Ich-1(I)'s enzymatic activity programmed cell	
CC	death can be inhibited, this may be useful in the development of new cell	
CC	lines which remain viable in culture for extended or indefinite periods,	
CC	independent of growth factors. (Updated on 25-MAR-2003 to correct PN	
CC	field.)	
SQ	Sequence 435 AA:	
XX		
XX	Query Match	27.9%; Score 210; DB 2; Length 435;
XX	Best Local Similarity	37.5%; Pred. No. 8.6e-15;
XX	Matches	42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;
OY	29 REGSEEDIDALEHMFROLFRESTMKRPDTAFQFDELEKFOQALDSDREDPVSCAFVYLMA 88	
DB	202 RSGGVVDHSTLVTFLKLGVDVHALCDQTAEOMOEKLONFAQ-LPAHRVTDSC-IVALLS 259	
OY	89 HGREGFLKGEDGEMWKLENLEPEALNNKNVCALRAKPXYITQACRGEORDPG 140	
DB	260 HGVEGATVGVDGSKLLQLQEVFPOLFDNANCPSLONKKMFFIQACRGDETDTG 311	
XX		
XX	RESULT 13	
XX	AAR98462	
XX	ID AAR98462 standard; protein; 435 AA.	
XX		
XX	AAR98462;	
XX		
DT	25-SEP-1996 (first entry)	
XX		
DE	Human Ice-ced-3 homologue-1L.	
XX		
KW	Ich-1L; human ICE-ced-3 homologue; programmed cell death; apoptosis;	
XX	interleukin-1 beta converting enzyme; gene therapy.	
OS	Homo sapiens.	
FX		
FX	Key	Location/Qualifiers
FT	Domain	301..305
FT		/label= QACRG_active_domain
XX		
PN	M09620721-AI.	
XX		
PD	11-JUL-1996.	
XX		
XX	04-JAN-1996;	96WO-US000177.
XX		
PR	04-JAN-1995;	95US-00368704.

```
XX (GEHO ) GEN HOSPITAL CORP.
XX
XX Yuan J, Miura M;
XX
XX WPI; 1996-333763/33.
XX N-PSDB; AAT31552.
XX
XX Preventing or promoting programmed cell death in vertebrate cells -
XX PT computes inhibiting or increasing the activity of interleukin-1-beta
XX PT converting enzyme, or altering expression of other related genes.
XX
XX Claim 19; Fig 10A; 127bp; English.
XX
XX A novel human cell death gene, designated Ich-1 (ICE-ced-3 homologue-1),
XX was identified as a new member of the ced-3/ICE family. Ich-1 is
XX alternatively spliced into 2 different forms. Ich-1L cDNA (AAT31552)
XX encodes a 435-amino acid protein (AAR98462) that is homologous to the P20
XX and P10 subunits of human interleukin-1 beta converting enzyme (ICE). Ich
XX -1S cDNA (AAT31553) encodes a 312-amino acid protein (AAR98463) that is a
XX truncated version of Ich-1L that terminates 21 residues after the QACRG
XX fibroblast cells to die in culture, but overexpression of Ich-1L induces Rat-1
XX suppresses Rat-1 cell death. Ich-1L and Ich-1S are useful in methods of
XX controlling programmed cell death of vertebrate cells
XX
XX Sequence 435 AA;
XX
XX Query Match 27.9%; Score 210; DB 2; Length 435;
XX Best Local Similarity 37.5%; Pred. No. 8.6e-15;
XX Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;
XX
XX 29 REGSEEDLALIEHMFRLQFESTMKRDPETAQFOEELKFOQALDSREDPVSCAFVIMA 88
XX Db 202 RSGGDVHSTLVTLFKLLGVVHVLCDQTAGMEQEKLNFAQ LPAHRVTDSC-IVALIS 259
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XX 89 HGRBGFLEKDEGVKLENIPEALNNKQCALRAKPKVYIITQACRGQRDPG 140
XX Db 260 HGVEGALYGVGKLLQLQEVFOLFEDNANCPSTLQNKPKMFFLQACRGDETDG 311
XX
XX RESULT 14
XX AAR90703
XX ID AAR90703 standard; protein; 435 AA.
XX
XX AC AAR90703;
XX
XX DT 10-APR-1996 (first entry)
XX
XX DE Interleukin-1-beta converting enzyme like apoptosis protease-2.
XX
XX KW Interleukin-1-beta converting enzyme like apoptosis protease-2;
XX KW ICE-LAP-2; cell death; immunosuppression; AIDS; Alzheimer disease;
XX KW Parkinson disease; septic shock; rheumatoid arthritis; head injury;
XX KW antitumor; antiviral.
XX
XX OS Homo sapiens.
XX
XX PN WO9600297-A1.
XX
XX PD 04-JAN-1996.
XX
XX PF 23-JUN-1994; 94WO-US007127.
XX
XX PR 23-JUN-1994; 94WO-US007127.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Wei WH, Craig AR, Hastings GA, Hudson PL, Kirkness EF;
XX
XX WPI; 1996-068881/07.
XX
XX N-PSDB; AAT15579.
XX
```

```
PT Interleukin-1 beta converting enzyme like apoptosis protease-1 and -2 -
PT controls programmed cell death, used in treatment of immunosuppression
PT related disorders, e.g. AIDS and Alzheimer's disease.
XX
XX Claim 1; Fig 2A-C; 58bp; English.
XX
XX Human interleukin-1-beta converting enzyme like apoptosis protease-2 (ICE
XX -LAP-2) (AAR90703) is structurally related interleukin-1-beta converting
XX enzyme, which is responsible for apoptosis. Recombinant ICE-LAP-2 is
XX obd. by expression of encoding cDNA (AAT15579) in prokaryotic or
XX eucaryotic host cells. It is used to treat diseases related to abnormally
XX controlled programmed cell death, to control vertebrate development and
XX tissue homeostasis, to overcome viral infections and to treat
XX immunosuppression-related disorders
XX
XX Sequence 435 AA;
XX
XX Query Match 27.9%; Score 210; DB 2; Length 435;
XX Best Local Similarity 37.5%; Pred. No. 8.6e-15;
XX Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;
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XX 29 REGSEEDLALIEHMFRLQFESTMKRDPETAQFOEELKFOQALDSREDPVSCAFVIMA 88
XX Db 202 RSGGDVHSTLVTLFKLLGVVHVLCDQTAGMEQEKLNFAQ LPAHRVTDSC-IVALIS 259
XX
XX 89 HGRBGFLEKDEGVKLENIPEALNNKQCALRAKPKVYIITQACRGQRDPG 140
XX Db 260 HGVEGALYGVGKLLQLQEVFOLFEDNANCPSTLQNKPKMFFLQACRGDETDG 311
XX
XX RESULT 15
XX AAM26274
XX ID AAM26274 standard; protein; 435 AA.
XX
XX AC AAM26274;
XX
XX DT 14-APR-1998 (first entry)
XX
XX DE Cell death protein ICH-11.
XX
XX KW cell death; ICH-11; interleukin-1 beta; apoptosis; treatment; IL-1;
XX KW tumour; oncogenic transformation; IL-1 receptor antagonist; IL-1Ra;
XX KW IL-1 beta.
XX
XX OS Homo sapiens.
XX
XX PN WO9733606-A1.
XX
XX PD 18-SEP-1997.
XX
XX PF 15-MAR-1996; 96WO-US003468.
XX
XX PR 15-MAR-1996; 96WO-US003468.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Yuan J, Friedlander R;
XX
XX WPI; 1997-470641/43.
XX
XX N-PSDB; AAT90565.
XX
XX Preventing apoptosis by blocking binding of interleukin-1beta to its
XX PT receptor - useful for, e.g. treating tumours, and inhibiting oncogenic
XX PT transformation.
XX
XX Example 5; Fig 7; 42bp; English.
XX
XX This is a cell death protein ICH-11. The cell death caused by this ICH-11
XX can be prevented by a new method using IL-1 receptor antagonist (IL-1Ra).
XX IL-1Ra is also used in a method for preventing programmed cell death by
XX blocking the binding of interleukin-1 beta (IL-1 beta) to its receptor.
XX Other methods for modulating programmed cell death are provided in the
XX specification like a method of modulating apoptosis by activating the IL-
```

CC 1 beta converting enzyme (ICE) pathway and IL-1 beta production, a method
 CC for altering levels of hypoxia-induced cell death by blocking IL-1-
 CC mediated signal transduction, a method for killing oncogenically
 CC transformed cells by stimulating apoptosis with IL-1 beta or tumour
 CC necrosis factor alpha (TNF alpha), a method of inhibiting hypoxia-induced
 CC cell death by transfecting cells with the CrmA gene (of compox), and a
 CC method for modulating apoptosis by downregulating the IL-1 receptor. IL-
 CC 1Ra inhibits apoptosis induced by trophic factor depletion or hypoxia,
 CC while mature IL-1 beta induces cell death through a pathway independent
 CC of CrmA-sensitive gene activity, and cooperates with ICE and ICH-1L in
 CC apoptosis. Pro-IL-1 beta is the first substrate of any apoptosis-inducing
 CC gene. Increasing/decreasing cells death can be used for the treatment of
 CC tumours (or other conditions where apoptosis is involved). Altering cell
 CC death can also be used for inhibiting oncogenic transformation, and to
 CC treat complications involving apoptosis in cases of hypoxia or ischaemia.
 CC The methods can also be used to screen for agents that modulate
 CC apoptosis. When IL-1 beta is produced endogenously (via ICE) it mediates
 CC cell death, but when added exogenously it may stimulate death if it binds
 CC to its receptor after application of apoptotic stimulus or inhibit it by
 CC binding to the receptor before application of the stimulus
 CC
 XX
 SQ Sequence 435 AA;

Query Match 27.9%; Score 210; DB 2; Length 435;
 Best Local Similarity 37.5%; Pred. No. 8.6e-15;
 Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;
 QY 29 REGSEEDLDALHEMFRLRFESTMTKRDPTAEQFOEBLEKFOQAIDSRDEPVSQAFVYVMA 68
 DB 202 RSGGDVDSHTVTLFTLGLGVAVVLCDOQAQEMQEKLNQFAQ-LFAHRYTDSQ-IVALLS 259
 QY 89 HGREGFLKGEDEGMVLENIFFAALNNKCOALRAKPKVYIIQACRGEQRPDG 140
 DB 260 HGEVGAIVGVGDKILOEVEVQLFDNANCPSLQNKPKMFFIIQACRGDETDG 311

Search completed: July 12, 2004, 13:47:47
 Job time : 44.438 secs

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CM protein - protein search, using sw model

Run on: July 12, 2004, 13:45:17 ; Search time 12.6694 Seconds
(without alignments)
594.928 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146

Perfect score: 752
Sequence: 1 MSNPRSLSEKXYDMSGAAL.....YIIQAKRGQRDPGTGGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	752	100.0	242	4	US-09-187-789-5	Sequence 5, Appli
2	747	99.3	230	4	US-09-187-789-7	Sequence 7, Appli
3	586	77.9	260	4	US-09-187-789-2	Sequence 2, Appli
4	586	77.9	260	4	US-09-139-600-2	Sequence 2, Appli
5	578	76.9	214	4	US-09-187-789-9	Sequence 9, Appli
6	293	39.0	74	4	US-09-187-789-63	Sequence 63, Appli
7	293	39.0	74	4	US-09-139-600-58	Sequence 58, Appli
8	210	27.9	421	4	US-08-983-502-10	Sequence 10, Appli
9	210	27.9	421	4	US-09-516-747-10	Sequence 10, Appli
10	210	27.9	421	5	PCT-US96-10521-10	Sequence 10, Appli
11	210	27.9	435	3	US-08-258-287B-53	Sequence 53, Appli
12	210	27.9	435	3	US-08-368-704C-51	Sequence 51, Appli
13	210	27.9	435	4	US-09-561-756-9	Sequence 9, Appli
14	210	27.9	435	4	US-09-227-721-9	Sequence 9, Appli
15	210	27.9	435	4	US-08-816-075-2	Sequence 2, Appli
16	210	27.9	435	4	US-08-724-378D-9	Sequence 9, Appli
17	210	27.9	435	4	US-09-954-697-9	Sequence 9, Appli
18	210	27.9	435	5	PCT-US94-07127A-4	Sequence 4, Appli
19	210	27.9	441	3	US-08-258-287B-44	Sequence 44, Appli
20	210	27.9	441	3	US-08-368-704C-43	Sequence 43, Appli
21	206	27.4	435	4	US-09-291-289-10	Sequence 10, Appli
22	197	26.2	312	3	US-08-258-287B-55	Sequence 55, Appli
23	197	26.2	312	3	US-08-368-704C-53	Sequence 53, Appli
24	190	25.3	56	4	US-09-187-789-64	Sequence 64, Appli
25	190	25.3	56	4	US-09-139-600-59	Sequence 59, Appli
26	189	25.1	404	4	US-09-445-724B-4	Sequence 4, Appli
27	189	25.1	404	4	US-09-445-724B-8	Sequence 8, Appli

28	187.5	24.9	311	2	US-08-391-916A-6	Sequence 6, Appli
29	187.5	24.9	383	2	US-08-391-916A-4	Sequence 4, Appli
30	187.5	24.9	404	1	US-08-203-716-2	Sequence 2, Appli
31	187.5	24.9	404	1	US-08-242-663A-2	Sequence 2, Appli
32	187.5	24.9	404	1	US-08-440-179-2	Sequence 2, Appli
33	187.5	24.9	404	2	US-08-450-130A-1	Sequence 1, Appli
34	187.5	24.9	404	2	US-08-391-916A-2	Sequence 2, Appli
35	187.5	24.9	404	2	US-08-573-890-2	Sequence 2, Appli
36	187.5	24.9	404	3	US-08-450-362A-1	Sequence 1, Appli
37	187.5	24.9	404	3	US-08-954-536-18	Sequence 18, Appli
38	187.5	24.9	404	3	US-09-039-657-2	Sequence 2, Appli
39	187.5	24.9	404	3	US-08-748-547-2	Sequence 2, Appli
40	187.5	24.9	404	3	US-08-908-436-3	Sequence 3, Appli
41	187.5	24.9	404	3	US-09-248-179-2	Sequence 2, Appli
42	187.5	24.9	404	4	US-09-069-023-30	Sequence 30, Appli
43	187.5	24.9	404	4	US-09-561-756-6	Sequence 6, Appli
44	187.5	24.9	404	4	US-09-227-721-6	Sequence 6, Appli
45	187.5	24.9	404	4	US-08-983-502-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-09-187-789-5
; Sequence 5, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-5

Query Match 100.0%; Score 752; DB 4; Length 242;

Best Local Similarity 100.0%; Pred. No. 3.5e-81; Mismatches 0; Gaps 0;

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DB	61	FOEELKEFOALISREDPVSCAFVYLMHARGEGFLKGEDEMYKLEMLFEALNNKCOAL	120
QY	121	RAKPKYIIQAKRGQRDPGTGGD	146
DB	121	RAKPKYIIQAKRGQRDPGTGGD	146

RESULT 2
US-09-187-789-7
; Sequence 7, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C1
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-7
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Query Match
Best Local Similarity 99.3%; Score 747; DB 4; Length 230;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPPTAEQ 60
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DB 61 FOEELKFOQALDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGGEORDPGETVGGD 146
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RESULT 3
US-09-187-789-2
; Sequence 2, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-2
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Best Local Similarity 77.9%; Score 586; DB 4; Length 260;
Matches 111; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
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QY 61 FOEELKFOQALDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 120
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QY 121 RAKPKVYIIQACRGGEORDPGETVGGD 146
DB 128 RAKPKVYIIQACRGGEORDPGETVGGD 153
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RESULT 4
US-09-139-600-2
; Sequence 2, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
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; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-2
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Query Match
Best Local Similarity 77.9%; Score 586; DB 4; Length 260;
Matches 111; Conservative 18; Mismatches 17; Indels 0; Gaps 0;
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QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPPTAEQ 60
DB 8 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPPTAEQ 67
QY 61 FOEELKFOQALDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 120
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QY 121 RAKPKVYIIQACRGGEORDPGETVGGD 146
DB 128 RAKPKVYIIQACRGGEORDPGETVGGD 153
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RESULT 5
US-09-187-789-9
; Sequence 9, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-9
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Best Local Similarity 76.9%; Score 578; DB 4; Length 214;
Matches 117; Conservative 0; Mismatches 1; Indels 28; Gaps 1;
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DB 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPPTAEQ 34
QY 61 FOEELKFOQALDSRDPVSCAFVLMAGRGEGFLKGDGEMVYKLENTFEALNNKNCQAL 120
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QY 121 RAKPKVYIIQACRGGEORDPGETVGGD 146
DB 93 RAKPKVYIIQACRGGEORDPGETVGGD 118
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RESULT 6
US-09-187-789-63
; Sequence 63, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emed S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
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: CURRENT FILING DATE: 1998-11-06
: NUMBER OF SEQ ID NOS: 78
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 63
: LENGTH: 74
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-187-789-63

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Query Match	39.0%;	Score 293;	DB 4;	Length 74;
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Qy 28 AREGSEDDLDALHEMFRLRFESTMKRPTAQEQEELKEFGQALDSREDPVSCAFVLM 87
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Qy 88 AHGREGFLKGED 99
||| ||| ||| |||
Db 61 AHGEEGLKGED 72

RESULT 7
US-09-139-600-58
Continuation of US-09-139-600-58

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; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHOD OF USE
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 58
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-58

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Query Match	39.0%	Score 293;	DB 4;	Length 74;
Best Local Similarity	77.8%;	Pred. No. 2.1e-27;		
Matches	56;	Conservative	8;	Mismatches 8;
				Indels 0;
				Gaps 0;

[illegible]

QY	88 AHGREGLKGED	99
Db	61 AHGEEGLKGED	72

RESULT 8
 US-08-983-502-10
 ? Sequence 10, Application US/08983502
 ? Patent No. 6399327
 ?
 ? GENERAL INFORMATION:
 ?
 ? APPLICANT: DAVID WALLACH
 ?
 ? APPLICANT: MARK P. BOLDIN
 ?
 ? APPLICANT: TANYA M. GONCHAROV
 ?
 ? APPLICANT: VARY V. GOLITSKY
 ?
 ? TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
 ?
 ? TITLE OF INVENTION: AND OTHER PROTEINS
 ?
 ? NUMBER OF SEQUENCES: 34
 ?
 ? CORRESPONDENCE ADDRESS:
 ?
 ? ADDRESSEE: BROWDY AND NEIMARK
 ?
 ? STREET: 419 Seventh Street N.W., Ste. 300
 ?
 ? CITY: Washington
 ?
 ? STATE: D.C.
 ?
 ? COUNTRY: USA
 ?

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10521
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
PRIORITY NUMBER: 114 515

APPLICATION NUMBER: IL 114,613
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 114,086

APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
PRIORITY NUMBER: 115 310

APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
PRIOR APPLICATION DATA:
PRIORITY NUMBER: 116 588

APPLICATION NUMBER: IL 116,588
FILING DATE: 27-DEC-1995
PRIOR APPLICATION DATA:
PRIORITY NUMBER: 117,033

APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
Name: David

NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=15

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528

```

; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids

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TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-983-502-10

Query Match	27.9%	Score	210	DB 4	Length	421			
Best Local Similarity	37.5%	Pred. No.	1.8e-16						
Matches	42	Conservative	29	Mismatches	39	Indels	2	Gaps	2

Dy 29 REGSEEDLDALHEHMFOLFREFSTMKRDPDTAFCFOEEIELEKFOCAIDSDSEDPAVSCAFVVIMA 88
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 188 RSGGDVDHSTLVTLFKLLGVYHVLCDDTAQEMOEKLNFAQLPRAHRTDSC-IVALLS 245

Cy 89 HGRGFLKGEDGEWYKLNLFEALNNKKOQALRAKPVIYIQACRGEDRPDG 140
||| : ||| : : : : : ||| : ||| : ||| : ||| : |||
Db 246 HGVEGAIYGVDKLTQLQEVFQLFDNANCFSLQNKKMFIIQACRGDEIDRG 297

RESULT 9
US-09-516-747-10
; Sequence 10, Application US/09516747
; Patent No. 6586571
; GENERAL INFORMATION:
; APPLICANT: David WALLACH
; Mark P. BOLDIN
; Tanya M. GONCHAROV
; Yuri V. GOLTSSEV
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
; AND OTHER PROTEINS
; ;
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESS: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
;

[illegible]

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-258-287B-53

Query Match 27.9%; Score 210; DB 3; Length 435;

Best Local Similarity 37.5%; Pred. No. 1.9e-16; Mismatches 29; Indels 2; Gaps 2;

Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDDIALHEMFQRLFEFTMKRDPFAEQFOEELKFOQALDSREDPVSCAFVYMA 88
DB 202 RSGGDVDSHTLVTLFKLLGYDVHVLCDQTAQEMQEKLNFAQ-LPAHRYTDSG-IVALLS 259

QY 89 HGREGFLKGEDEGMVXENLFEALNNKQCALRAKPKVYIIQACRGQRDPG 140
DB 260 HVEGAIVGVGDKLLQLQEVFQLPDANCPSLQNKPKMFFIQACRGDETRDG 311

RESULT 12

US-08-368-704C-51
Sequence 51, Application US/08368704C
Patent No. 6087160

GENERAL INFORMATION:

APPLICANT: Yuan, Junying

APPLICANT: Mura, Masayuki

TITLE OF INVENTION: Programmed Cell Death Genes and Proteins

NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/368,704C

FILING DATE: 4-JAN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/080,850

FILING DATE: 24-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Bugalsky, Lawrence B.

REGISTRATION NUMBER: 35,086

REFERENCE/DOCKET NUMBER: 0609, 3920002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2540

TELEFAX: (202) 371-2540

TELEX: 248636 SSK

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 435 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-368-704C-51

Query Match 27.9%; Score 210; DB 3; Length 435;

Best Local Similarity 37.5%; Pred. No. 1.9e-16; Mismatches 29; Indels 2; Gaps 2;

Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDDIALHEMFQRLFEFTMKRDPFAEQFOEELKFOQALDSREDPVSCAFVYMA 88
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QY 89 HGREGFLKGEDEGMVXENLFEALNNKQCALRAKPKVYIIQACRGQRDPG 140
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RESULT 13

US-09-561-756-9
Sequence 9, Application US/09561756
Patent No. 6376226

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

FILE REFERENCE: 480140.431

CURRENT APPLICATION NUMBER: US/09/561,756

CURRENT FILING DATE: 2000-04-26

PRIOR APPLICATION NUMBER: 09/227,721

PRIOR FILING DATE: 1998-01-08

NUMBER OF SEQ ID NOS: 116

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 9

LENGTH: 435

TYPE: PRT

ORGANISM: Homo sapien

US-09-561-756-9

Query Match 27.9%; Score 210; DB 4; Length 435;

Best Local Similarity 37.5%; Pred. No. 1.9e-16; Mismatches 29; Indels 2; Gaps 2;

Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDDIALHEMFQRLFEFTMKRDPFAEQFOEELKFOQALDSREDPVSCAFVYMA 88
DB 202 RSGGDVDSHTLVTLFKLLGYDVHVLCDQTAQEMQEKLNFAQ-LPAHRYTDSG-IVALLS 259

QY 89 HGREGFLKGEDEGMVXENLFEALNNKQCALRAKPKVYIIQACRGQRDPG 140
DB 260 HVEGAIVGVGDKLLQLQEVFQLPDANCPSLQNKPKMFFIQACRGDETRDG 311

RESULT 14

US-09-227-721-9
Sequence 9, Application US/09227721
Patent No. 6379950

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

FILE REFERENCE: 480140.431

CURRENT APPLICATION NUMBER: US/09/227,721

CURRENT FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 116

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 9

LENGTH: 435

TYPE: PRT

ORGANISM: Homo sapien

US-09-227-721-9

Query Match 27.9%; Score 210; DB 4; Length 435;

Best Local Similarity 37.5%; Pred. No. 1.9e-16; Mismatches 29; Indels 2; Gaps 2;

Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDDIALHEMFQRLFEFTMKRDPFAEQFOEELKFOQALDSREDPVSCAFVYMA 88
DB 202 RSGGDVDSHTLVTLFKLLGYDVHVLCDQTAQEMQEKLNFAQ-LPAHRYTDSG-IVALLS 259

QY 89 HGREGFLKGEDEGMVXENLFEALNNKQCALRAKPKVYIIQACRGQRDPG 140
DB 260 HVEGAIVGVGDKLLQLQEVFQLPDANCPSLQNKPKMFFIQACRGDETRDG 311

RESULT 15

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US-08-816-075-2
: Sequence 2, Application US/08816075
: Patent No. 6416753
:
: GENERAL INFORMATION:
:
: APPLICANT: Yuan, Junying
: APPLICANT: Friedlander, Robert
: TITLE OF INVENTION: Programmed Cell Death and Interleukin-1
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STRANE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 New York Ave., N.W.
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/816,075
: FILING DATE: 13-MAR-1997
: CLASSIFICATION: 424
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/013,524
: FILING DATE: 15-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Bugalsky, Lawrence B.
: REGISTRATION NUMBER: 35,086
: REFERENCE/DOCKET NUMBER: 0609-421001/JAG/LBB
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 435 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
US-08-816-075-2

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:50:22 ; Search time 35.8967 Seconds
(without alignments)
1268.642 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146

Perfect score: 752
Sequence: 1 MSNPRSLSEKXDMGALAL.....YIIQACRGQRDPGETVGGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep.*
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18: /cgn2_6/prodata/2/pubppa/US60_NEW_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	752	100.0	242	9 US-09-989-903-5	Sequence 5, Appl1
2	752	100.0	242	14 US-10-068-564-5	Sequence 5, Appl1
3	747	99.3	174	15 US-10-114-432-34	Sequence 34, Appl1
4	747	99.3	230	9 US-09-989-903-7	Sequence 7, Appl1
5	747	99.3	230	14 US-10-068-564-7	Sequence 7, Appl1
6	747	99.3	230	15 US-10-114-432-5	Sequence 15, Appl1
7	747	99.3	230	15 US-10-114-432-19	Sequence 19, Appl1
8	747	99.3	230	15 US-10-114-432-64	Sequence 64, Appl1
9	747	99.3	230	15 US-10-114-432-68	Sequence 68, Appl1
10	747	99.3	242	9 US-09-845-028-2	Sequence 2, Appl1
11	747	99.3	242	10 US-09-851-873-105	Sequence 105, Appl1
12	747	99.3	242	15 US-10-114-432-3	Sequence 3, Appl1
13	747	99.3	242	15 US-10-114-432-15	Sequence 15, Appl1
14	747	99.3	242	15 US-10-114-432-17	Sequence 17, Appl1
15	747	99.3	242	15 US-10-114-432-18	Sequence 18, Appl1

16	747	99.3	242	15 US-10-114-432-26	Sequence 26, Appl1
17	747	99.3	242	15 US-10-114-432-27	Sequence 27, Appl1
18	747	99.3	242	15 US-10-114-432-28	Sequence 28, Appl1
19	747	99.3	242	15 US-10-114-432-30	Sequence 30, Appl1
20	747	99.3	242	15 US-10-114-432-31	Sequence 31, Appl1
21	747	99.3	242	15 US-10-114-432-67	Sequence 67, Appl1
22	747	99.3	242	15 US-10-114-432-69	Sequence 69, Appl1
23	747	99.3	242	15 US-10-114-432-71	Sequence 71, Appl1
24	747	99.3	242	15 US-10-114-432-73	Sequence 73, Appl1
25	745	99.1	242	15 US-10-114-432-13	Sequence 13, Appl1
26	745	99.1	242	15 US-10-114-432-33	Sequence 33, Appl1
27	742	98.7	241	15 US-10-114-432-37	Sequence 37, Appl1
28	735	97.7	242	15 US-10-114-432-11	Sequence 11, Appl1
29	735	97.7	242	15 US-10-114-432-22	Sequence 22, Appl1
30	713	94.8	241	15 US-10-114-432-36	Sequence 36, Appl1
31	713	94.8	321	15 US-10-114-432-9	Sequence 9, Appl1
32	713	94.8	321	15 US-10-114-432-21	Sequence 21, Appl1
33	713	94.8	321	15 US-10-114-432-66	Sequence 66, Appl1
34	713	94.8	321	15 US-10-114-432-72	Sequence 72, Appl1
35	707	94.0	242	9 US-09-764-803A-24	Sequence 24, Appl1
36	702	93.4	242	9 US-09-845-028-9	Sequence 9, Appl1
37	681	90.6	134	15 US-10-114-432-32	Sequence 32, Appl1
38	681	90.6	134	15 US-10-114-432-33	Sequence 33, Appl1
39	681	90.6	146	15 US-10-114-432-7	Sequence 7, Appl1
40	681	90.6	146	15 US-10-114-432-20	Sequence 20, Appl1
41	681	90.6	146	15 US-10-114-432-65	Sequence 65, Appl1
42	681	90.6	146	15 US-10-114-432-70	Sequence 70, Appl1
43	679	90.3	229	9 US-09-764-803A-4	Sequence 4, Appl1
44	586	77.9	185	15 US-10-114-432-35	Sequence 35, Appl1
45	586	77.9	253	15 US-10-114-432-29	Sequence 29, Appl1

ALIGNMENTS

RESULT 1
US-09-989-903-5
; Sequence 5, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emdad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434D
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-903-5

Query Match 100.0%; Score 752; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.2e-70; Indels 0; Gaps 0;
Matches 146; Conservative 0; Mismatches 0;

QY	1	MSNPRSLSEKXDMGALALILCVTKAREGSEEDLDALSHNERQLRFESTMKDPTAAQ	60
DB	1	MSNPRSLSEKXDMGALALILCVTKAREGSEEDLDALSHNERQLRFESTMKDPTAAQ	60
QY	61	FOEELKFKQALDSREDPVSCAFVYLMAGREGGLKEDGEMVYLENLFELANKNCAL	120
DB	61	FOEELKFKQALDSREDPVSCAFVYLMAGREGGLKEDGEMVYLENLFELANKNCAL	120
QY	121	RAKPKVYIIQACRGQRDPGETVGGD	146
DB	121	RAKPKVYIIQACRGQRDPGETVGGD	146

RESULT 2

US-10-068-564-5
; Sequence 5, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PR1
; ORGANISM: Homo sapien
US-10-068-564-5

Query Match 100.0%; Score 752; DB 14; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.2e-70;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNPSLEBEKYMDSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAEQ 60
DB 1 MSNPSLEBEKYMDSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAEQ 60
QY 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVLENTFEALNNKCOAL 120
DB 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVLENTFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146

RESULT 3
US-10-114-432-34
; Sequence 34, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobiwits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 174
; TYPE: PR1
; ORGANISM: Homo Sapiens
US-10-114-432-34

Query Match 99.3%; Score 747; DB 15; Length 174;
Best Local Similarity 99.3%; Pred. No. 4.7e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEBEKYMDSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAEQ 60
DB 1 MSNPSLEBEKYMDSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAEQ 60
QY 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVLENTFEALNNKCOAL 120
DB 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVLENTFEALNNKCOAL 120

QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146

RESULT 4
US-09-989-903-7
; Sequence 7, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 230
; TYPE: PR1
; ORGANISM: Homo sapien
US-09-989-903-7

Query Match 99.3%; Score 747; DB 9; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEBEKYMDSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAEQ 60
DB 1 MSNPSLEBEKYMDSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAEQ 60
QY 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVLENTFEALNNKCOAL 120
DB 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVLENTFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146

RESULT 5
US-10-068-564-7
; Sequence 7, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 230
; TYPE: PR1
; ORGANISM: Homo sapien
US-10-068-564-7

Query Match 99.3%; Score 747; DB 14; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPSLEBEKYMDSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAEQ 60
DB 1 MSNPSLEBEKYMDSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAEQ 60
QY 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVLENTFEALNNKCOAL 120
DB 61 FOELEKFOQAIDSRDPVSCAFVVLMAHGREGFLKGEDGEMVLENTFEALNNKCOAL 120

Db 61 FOEIELEKFOQAIDSREDVSCAFVYLMHGREBFLKGEDGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGGEORDPGETVGD 146
Db 121 RAKPKVYIIQACRGGEORDPGETVGD 146

RESULT 6
US-10-114-432-5
; Sequence 5, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1I1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-5

Query Match 99.3%; Score 747; DB 15; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARBSSEDDALHEHMRQRLFEESTMKRDPYAEQ 60
Db 1 MSNPRSLSEEEKYDMSGARLALILCVTKARBSSEDDALHEHMRQRLFEESTMKRDPYAEQ 60
QY 61 FOEIELEKFOQAIDSREDVSCAFVYLMHGREBFLKGEDGEMVKLENLFEALNNKCOAL 120
Db 61 FOEIELEKFOQAIDSREDVSCAFVYLMHGREBFLKGEDGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGGEORDPGETVGD 146
Db 121 RAKPKVYIIQACRGGEORDPGETVGD 146

RESULT 7
US-10-114-432-19
; Sequence 19, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1I1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 230
; TYPE: PRT

; ORGANISM: Homo Sapiens
US-10-114-432-19
Query Match 99.3%; Score 747; DB 15; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARBSSEDDALHEHMRQRLFEESTMKRDPYAEQ 60
Db 1 MSNPRSLSEEEKYDMSGARLALILCVTKARBSSEDDALHEHMRQRLFEESTMKRDPYAEQ 60
QY 61 FOEIELEKFOQAIDSREDVSCAFVYLMHGREBFLKGEDGEMVKLENLFEALNNKCOAL 120
Db 61 FOEIELEKFOQAIDSREDVSCAFVYLMHGREBFLKGEDGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGGEORDPGETVGD 146
Db 121 RAKPKVYIIQACRGGEORDPGETVGD 146

RESULT 8
US-10-114-432-64
; Sequence 64, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1I1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-64

Query Match 99.3%; Score 747; DB 15; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARBSSEDDALHEHMRQRLFEESTMKRDPYAEQ 60
Db 1 MSNPRSLSEEEKYDMSGARLALILCVTKARBSSEDDALHEHMRQRLFEESTMKRDPYAEQ 60
QY 61 FOEIELEKFOQAIDSREDVSCAFVYLMHGREBFLKGEDGEMVKLENLFEALNNKCOAL 120
Db 61 FOEIELEKFOQAIDSREDVSCAFVYLMHGREBFLKGEDGEMVKLENLFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGGEORDPGETVGD 146
Db 121 RAKPKVYIIQACRGGEORDPGETVGD 146

RESULT 9
US-10-114-432-68
; Sequence 68, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.

```
APPLICANT: Ge, Wangmao
APPLICANT: Jakobivits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 68
LENGTH: 230
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-68
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Query Match 99.3%; Score 747; DB 15; Length 230;
Best Local Similarity 99.3%; Pred. No. 6.8e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
DB 1 MSNPSLEEEKYDMSGARLALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
QY 61 FOEBLEKFOQAIDSREDPVSCAFVYIMAHGREGFLKGEDEGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEBLEKFOQAIDSREDPVSCAFVYIMAHGREGFLKGEDEGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146
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RESULT 10
US-09-845-028-2
; Sequence 2, Application US/09845028
; Patent No. US20020081705A1
; GENERAL INFORMATION:
; APPLICANT: Markovitch, John
; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
; FILE REFERENCE: BBI-111
; CURRENT APPLICATION NUMBER: US/09/845,028
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199,962
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-028-2

Query Match 99.3%; Score 747; DB 9; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
DB 1 MSNPSLEEEKYDMSGARLALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
QY 61 FOEBLEKFOQAIDSREDPVSCAFVYIMAHGREGFLKGEDEGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEBLEKFOQAIDSREDPVSCAFVYIMAHGREGFLKGEDEGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146
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RESULT 11
US-09-851-873-105
; Sequence 105, Application US/09851873

```
Publication No. US20030165488A1
GENERAL INFORMATION:
APPLICANT: Kleczien, Rolf F
APPLICANT: Reardon, Ilene M
APPLICANT: Weiland, Katherine L
TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
FILE REFERENCE: 28341/0023
CURRENT APPLICATION NUMBER: US/09/851,873
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
US-09-851-873-105
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Query Match 99.3%; Score 747; DB 10; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
DB 1 MSNPSLEEEKYDMSGARLALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
QY 61 FOEBLEKFOQAIDSREDPVSCAFVYIMAHGREGFLKGEDEGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEBLEKFOQAIDSREDPVSCAFVYIMAHGREGFLKGEDEGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
DB 121 RAKPKVYIIQACRGQRDPGETVGGD 146
```

RESULT 12
US-10-114-432-3
; Sequence 3, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chalilta-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-3

Query Match 99.3%; Score 747; DB 15; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSNPSLEEEKYDMSGALALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
DB 1 MSNPSLEEEKYDMSGARLALILCVTKAREGSEEDLDALHEMFROLRFESTMKRDPPTAQ 60
QY 61 FOEBLEKFOQAIDSREDPVSCAFVYIMAHGREGFLKGEDEGEMVKLENLFEALNNKNCQAL 120
DB 61 FOEBLEKFOQAIDSREDPVSCAFVYIMAHGREGFLKGEDEGEMVKLENLFEALNNKNCQAL 120
QY 121 RAKPKVYIIQACRGQRDPGETVGGD 146
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Db 121 RAKPKVYIIQACRGGEQRPGETVGGD 146

RESULT 13

US-10-114-432-15
; Sequence 15, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-15

Query Match 99.3%; Score 747; DB 15; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYMSGALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
DB 1 MSNPRLSEEEKYMSGARLALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
QY 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGBGFLKGEDEMYKLENTLFEALNNKCOAL 120
DB 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGBGFLKGEDEMYKLENTLFEALNNKCOAL 120

QY 121 RAKPKVYIIQACRGGEQRPGETVGGD 146
DB 121 RAKPKVYIIQACRGGEQRPGETVGGD 146

RESULT 14

US-10-114-432-17
; Sequence 17, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-17

Query Match 99.3%; Score 747; DB 15; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYMSGALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
DB 1 MSNPRLSEEEKYMSGARLALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
QY 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGBGFLKGEDEMYKLENTLFEALNNKCOAL 120
DB 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGBGFLKGEDEMYKLENTLFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGGEQRPGETVGGD 146
DB 121 RAKPKVYIIQACRGGEQRPGETVGGD 146

RESULT 15

US-10-114-432-18
; Sequence 18, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-18

Query Match 99.3%; Score 747; DB 15; Length 242;
Best Local Similarity 99.3%; Pred. No. 7.3e-70;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRLSEEEKYMSGALALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
DB 1 MSNPRLSEEEKYMSGARLALILCVTKARSGSEEDLDALHMFROLRFESTMKRDPYAEQ 60
QY 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGBGFLKGEDEMYKLENTLFEALNNKCOAL 120
DB 61 FOELEKFOQAIDSREDPVSCAFVVLMAHGBGFLKGEDEMYKLENTLFEALNNKCOAL 120
QY 121 RAKPKVYIIQACRGGEQRPGETVGGD 146
DB 121 RAKPKVYIIQACRGGEQRPGETVGGD 146

Search completed: July 12, 2004, 14:04:00
Job time : 35.8967 secs

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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:44:06 ; Search time 10.5579 Seconds
(without alignments)
1330.191 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146

Perfect score: 752
Sequence: 1 MSNPRSLSEKXYDMSGALAL.....YIIQACRGGRDPGETVGGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	747	99.3	242	2 JC7517	caspase-14/a - hum
2	210	27.9	435	2 A54821	apoptosis regulato
3	205	27.3	182	2 I67436	interleukin-1-beta
4	205	27.3	452	2 JC6587	caspase-2 - rat
5	197	26.2	312	2 B54821	apoptosis regulato
6	194	25.8	454	2 JC7123	caspase-9 long cha
7	187.5	24.9	311	2 B56084	interleukin-1beta
8	187.5	24.9	383	2 A56084	interleukin-1beta
9	187.5	24.9	404	2 A42677	interleukin-1beta
10	185.5	24.7	263	2 C56084	interleukin-1beta
11	179.5	23.9	277	2 A55315	cysteine proteinas
12	175	23.3	418	2 B57511	interleukin-1 beta
13	174.5	23.0	212	2 I67437	cysteine proteinas
14	173	23.0	402	2 A46495	IF-1 beta converta
15	171.5	22.8	277	2 JC5410	CPP32 protein - mo
16	168.5	22.4	277	2 B54710	cysteine proteinas
17	168	22.3	377	2 A57511	interleukin-1 beta
18	167	22.2	416	2 G02635	ICE-LAP6 - human
19	151	20.1	495	2 T20038	hypothetical prote
20	151	20.1	503	2 A49429	interleukin-1 beta
21	132	17.6	826	2 T43638	caspase-related pr
22	127.5	17.0	136	2 I53300	interleukin-1-beta
23	94.5	12.6	536	2 T43633	caspase-related pr
24	92	12.2	1313	2 A48467	myosin heavy chain
25	89.5	11.9	642	2 T27021	hypothetical prote
26	88.5	11.8	149	2 T43637	caspase protein 1C
27	84.5	11.2	520	2 F70350	recombination prot
28	82.5	11.0	167	2 S70824	hypothetical prote
29	82	10.9	1957	2 A45627	myosin heavy chain

30	81.5	10.8	484	2 F81859	conserved hypothet
31	81.5	10.8	484	2 F81083	conserved hypothet
32	79	10.5	676	2 S00084	myosin heavy chain
33	79	10.5	918	2 C96829	unknown protein F1
34	79	10.5	1957	2 A59294	skeletal myosin -
35	78	10.4	510	2 S42626	ER-golgi intermedi
36	78	10.4	1389	2 T41230	hypothetical TPR d
37	77	10.2	354	2 B75003	hypothetical prote
38	77	10.2	599	2 G83941	ABC transporter (A
39	77	10.2	906	2 G89531	alanyl-tRNA synthet
40	77	10.2	1225	2 A56514	chromokinesin - ch
41	77	10.2	1265	2 T07397	kinasin heavy chain
42	76.5	10.2	415	2 C35760	fcra protein precu
43	76.5	10.2	468	1 TWMS2	transcription fact
44	76	10.1	154	2 B81866	conserved hypothet
45	76	10.1	627	2 A69663	DNA mismatch repai

ALIGNMENTS

RESULT 1

JC7517
caspase-14/a - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C/Accession: JC7517
R/Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.
Biochem. Biophys. Res. Commun. 277, 655-659, 2000
A/Title: Caspase-14: Analysis of gene structure and mRNA expression during keratinocyte
A/Reference number: JC7517; PMID:20517231; PMID:11062009
A/Contents: Epidermal keratinocytes
A/Accession: JC7517
A/Molecule type: mRNA
A/Residues: 1-242 <ECK>
A/Cross-references: GB:AF097874
C/Comment: This enzyme accumulates during keratinocyte differentiation and is activate
C/Genetics:
A/Gene: casp-14/a
A/Map position: 19p13.1
A/Introns: 9/3; 59/3; 135/1; 174/1; 208/3
C/Keywords: differentiation

Query Match	Score	DB 2:	Length	242:
Best Local Similarity	99.3%	Pred. No. 1.1e-57;		
Matches 145; Conservative	0;	Mismatches 1;	Indels	0; Gaps 0;
QY	1	MSNPRSLSEKXYDMSGALALILCVTKARSGSEDDDALHMFROLFESTMKRPTAAQ	60	
DB	1	MSNPRSLSEKXYDMSGARLILCVTKARSGSEDDDALHMFROLFESTMKRPTAAQ	60	
QY	61	FOELEKFOQALDSREDDVSCAFVIMAHGRBEGFLKGEDEMYKLEMLFEALNNKCOAL	120	
DB	61	FOELEKFOQALDSREDDVSCAFVIMAHGRBEGFLKGEDEMYKLEMLFEALNNKCOAL	120	
QY	121	RAKPKXYIIQACRGGRDPGETVGGD	146	
DB	121	RAKPKXYIIQACRGGRDPGETVGGD	146	

RESULT 2

A54821
apoptosis regulator ICH-1, stimulatory form L - human
C/Species: Homo sapiens (man)
C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C/Accession: A54821
R/Wang, L.; Minura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78, 739-750, 1994
A/Title: Ich-1, an ice/ced-3-related gene, encodes both positive and negative regulato
A/Reference number: A54821; PMID:94373811; PMID:8087842
A/Accession: A54821
A/Status: preliminary
A/Molecule type: mRNA

A;Residues: 1-435 <MAN>
A;Cross-references: GB:U13021; NID:9537291; PID:9537292
C;Keywords: alternative splicing; apoptosis

Query Match 27.9%; Score 210; DB 2; Length 435;
Best Local Similarity 37.5%; Pred. No. 9.4e-11;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHEMFROLFEFTMKRDPPTAEOFOEELKFOQAIDSREDPVSCAFVYMA 88
Db 202 RSGGDVHSTLVTTLFKLGVVHVHLCDTAQMOKLQNFQO-LPAHRTDSC-IVALIS 259
QY 89 HGRGFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEORDPG 140
Db 260 HGVGALIVGDGKLQLOEVFRLFDNANCPSLQNKPKMFFIQACRGEORDPG 311

RESULT 3

167436
interleukin-1-beta-converting enzyme and ced-3 homolog-1, long isoform - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: 167436
R;Flaws: J.A.; Kugu, K.; Tihovich, A.M.; Desanti, A.; Tilly, K.I.; Hirschfeld, A.N.; Til
Endocrinology 136; 5042-5053, 1995
A;Title: Interleukin-1-beta-converting enzyme-related proteases (IRPs) and mammalian cel
nuclea cells of the ovarian follicle.
A;Reference number: 153300; MUID:96042508; PMID:7588240
A;Accession: 167436
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-182 <RSS>
A;Cross-references: EMBL:U34684; NID:g1004368; PID:AA052260.1; PID:g1004369

Query Match 27.3%; Score 205; DB 2; Length 182;
Best Local Similarity 37.5%; Pred. No. 9.6e-11;
Matches 42; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHEMFROLFEFTMKRDPPTAEOFOEELKFOQAIDSREDPVSCAFVYMA 88
Db 22 RSGGDVHSTLVTTLFKLGVVHVHLCDTAQMOKLQNFQO-LPAHRTDSC-IVALIS 79
QY 89 HGRGFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEORDPG 140
Db 80 HGVGALIVGDGKLQLOEVFRLFDNANCPSLQNKPKMFFIQACRGEORDPG 131

RESULT 4

JC6507
Caspase-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: JC6507
R;Sato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.
Gene 202; 121-132, 1997
A;Title: Cloning and expression of the cDNA encoding rat caspase-2.
A;Reference number: JC6507; MUID:98087427; PMID:9427555
A;Accession: JC6507
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-452 <SAT>
A;Cross-references: GB:U07933; NID:g2769705; PID:AA063379.1; PID:g2769706

Query Match 27.3%; Score 205; DB 2; Length 452;
Best Local Similarity 37.5%; Pred. No. 2.7e-10;
Matches 42; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHEMFROLFEFTMKRDPPTAEOFOEELKFOQAIDSREDPVSCAFVYMA 88
Db 219 RSGGDVHSTLVTTLFKLGVVHVHLCDTAQMOKLQNFQO-LPAHRTDSC-IVALIS 276
QY 89 HGRGFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEORDPG 140

Db 277 HGVGALIVGDGKLQLOEVFRLFDNANCPSLQNKPKMFFIQACRGEORDPG 328

RESULT 5

B54821
apoptosis regulator ICH-1, suppressive form S - human
C;Species: Homo sapiens (man)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C;Accession: B54821
R;Wang, L.; Mura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
Cell 78; 739-750, 1994
A;Title: Ich-1, an Ice/ced-3-related gene, encodes both positive and negative regulator
A;Reference number: B54821; MUID:94373811; PMID:8087842
A;Accession: B54821
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-312 <MAN>
A;Cross-references: GB:U10322
C;Keywords: alternative splicing; apoptosis

Query Match 26.2%; Score 197; DB 2; Length 312;
Best Local Similarity 37.7%; Pred. No. 8.7e-10;
Matches 40; Conservative 27; Mismatches 37; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHEMFROLFEFTMKRDPPTAEOFOEELKFOQAIDSREDPVSCAFVYMA 88
Db 188 RSGGDVHSTLVTTLFKLGVVHVHLCDTAQMOKLQNFQO-LPAHRTDSC-IVALIS 245
QY 89 HGRGFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACR 134
Db 246 HGVGALIVGDGKLQLOEVFRLFDNANCPSLQNKPKMFFIQACR 291

RESULT 6

JC7123
caspase-9 long chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Accession: JC7123
R;Fujita, E.; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264; 550-555, 1999
A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
A;Reference number: JC7123; MUID:20001956; PMID:10529400
A;Accession: JC7123
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-454 <PU>
A;Cross-references: DBJ:AB019600; NID:g6440941; PID:g6440942

Query Match 25.8%; Score 194; DB 2; Length 454;
Best Local Similarity 37.4%; Pred. No. 2.4e-09;
Matches 46; Conservative 17; Mismatches 42; Indels 18; Gaps 3;

QY 29 REGSEEDLDALHEMFROLFEFTMKRDPPTAEOFOEELKFOQAIDSREDPVSCAFV 84
Db 218 RSGSNIDRKLHRRRMVPMVAVKNDLTAKKVNTALMAHNNRHALD-----CFVV 270
QY 85 VIMAGRE-----GFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYIIQACRGEOR 137
Db 271 VILSHGQASHLQFGAVVGTGCSVSIKIVNFNGSGCPGLGKPKLFFIQACGGEOR 330
QY 138 DRG 140
Db 331 DRG 333

RESULT 7

B56084
interleukin-1beta converting enzyme gamma isozyyme - human
C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
C;Accession: B56084
R;Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.

J. Biol. Chem. 270, 4312-4317, 1995
 A>Title: Cloning and expression of four novel isoforms of human interleukin-1beta converting enzyme
 A:Reference number: A56084; MUID:95181414; PMID:7876192
 A:Accession: B56084
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-311 <ALN>
 A:Cross-references: GB:U13698; NID:9717041; PIDN:AAC50108.1; PID:9717042
 C:Genetics:
 A:Gene: IL1BCE
 C:Keywords: alternative splicing

Query Match 24.9%; Score 187.5; DB 2; Length 311;
 Best Local Similarity 35.2%; Pred. No. 5.8e-09;
 Matches 51; Conservative 23; Mismatches 52; Indels 19; Gaps 6;

Db 67 SGAAALILICVTK-----AREGSEEDLDLEHMFRLPFSITMKRDPPTAQQFOEELKFKQ 69
 15 SGAAALILICVTK-----AREGSEEDLDLEHMFRLPFSITMKRDPPTAQQFOEELKFKQ 69
 67 SRTRLALITCNEEDSDIPRTGAEVDITGWTMLQNGSVYKKNLTASDMTELEAFA 126
 Qy 70 QAIDSRDPVSCAFVYIMAHG-REGFLKSGEDGMV-----KLENI,FEALNNKNCQALRAKP 124
 127 HREPHKTS--DSTFLVFMHSHGIRREGICGKHSQVDPDIQLNMFNMLTKNCPSLKDKP 184
 Db 125 KYVITIQACRGEQDPG-----ETVG 144
 185 KVIITIQACRGD--SPGVWFKDSVG 207

RESULT 8
 A56084
 interleukin-1beta converting enzyme beta isozyme - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
 C:Accession: A56084
 R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
 J. Biol. Chem. 270, 4312-4317, 1995
 A>Title: Cloning and expression of four novel isoforms of human interleukin-1beta converting enzyme
 A:Reference number: A56084; MUID:95181414; PMID:7876192
 A:Accession: A56084
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-383 <ALN>
 A:Cross-references: GB:U13697; NID:9717039; PIDN:AAC50107.1; PID:9717040
 C:Genetics:
 A:Gene: IL1BCE
 C:Keywords: alternative splicing

Query Match 24.9%; Score 187.5; DB 2; Length 383;
 Best Local Similarity 35.2%; Pred. No. 7.3e-09;
 Matches 51; Conservative 23; Mismatches 52; Indels 19; Gaps 6;

Qy 15 SGAAALILICVTK-----AREGSEEDLDLEHMFRLPFSITMKRDPPTAQQFOEELKFKQ 69
 Db 139 SRTRLALITCNEEDSDIPRTGAEVDITGWTMLQNGSVYKKNLTASDMTELEAFA 198
 Qy 70 QAIDSRDPVSCAFVYIMAHG-REGFLKSGEDGMV-----KLENI,FEALNNKNCQALRAKP 124
 Db 199 HREPHKTS--DSTFLVFMHSHGIRREGICGKHSQVDPDIQLNMFNMLTKNCPSLKDKP 256
 Qy 125 KYVITIQACRGEQDPG-----ETVG 144
 Db 257 KVIITIQACRGD--SPGVWFKDSVG 279

RESULT 9
 A42677
 interleukin-1 beta converting enzyme (EC 3.4.22.-) - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: A54263; A42677; S21734; S24164
 R:Carrettii, D.P.; Hollingsworth, L.T.; Kozlosky, C.J.; Valentine, M.B.; Shapiro, D.N.; M
 Genomics 20, 468-473, 1994

A>Title: Molecular characterization of the gene for human interleukin-1beta converting
 A:Reference number: A54263; MUID:94307734; PMID:8034320
 A:Accession: A54263
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-404 <CE2>
 A:Cross-references: GB:I27475
 R:Carrettii, D.P.; Kozlosky, C.J.; Mosley, B.; Nelson, N.; Van Ness, K.; Greenstreet, T
 Science 256, 97-100, 1992
 A>Title: Molecular cloning of the interleukin-1beta converting enzyme.
 A:Reference number: A42677; MUID:92229430; PMID:1373520
 A:Accession: A42677
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-404 <CE2>
 A:Cross-references: GB:M87507; NID:9435598; PIDN:AAA66942.1; PID:9186286
 R:Chomberg, N.A.; Bull, H.G.; Calaycay, J.R.; Chapman, K.T.; Howard, A.D.; Kostruta, N
 J. Dng, G.C.F.; Egger, L.A.; Gaffney, E.P.; Limuoco, G.; Palyha, O.C.; Raju, S.M.; R
 cci, M.J
 Nature 356, 768-774, 1992

A>Title: A novel heterodimeric cysteine protease is required for interleukin-1beta pro
 A:Reference number: S21734; MUID:92244338; PMID:1574116
 A:Accession: S21734
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-404 <THO>
 A:Cross-references: EMBL:X65019; NID:933792; PIDN:CAA46153.1; PID:933793
 R:Kronheim, S.R.; Muma, A.; Greenstreet, T.; Glackin, P.J.; van Ness, K.; March, C.J.
 Arch. Biochem. Biophys. 296, 698-703, 1992
 A>Title: Purification of interleukin-1beta converting enzyme, the protease that cleave
 A:Reference number: S24164; MUID:92337439; PMID:1321594
 A:Accession: S24164
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 120-135,'AX',138-139,'X',141-142 <KRO>
 A:Gene: GDB:IL1BC
 A:Cross-references: GDB:132368; OMIM:147678
 A:Map position: 11q23-11q23
 C:Keywords: cysteine proteinase; hydrolase

Query Match 24.9%; Score 187.5; DB 2; Length 404;
 Best Local Similarity 35.2%; Pred. No. 7.8e-09;
 Matches 51; Conservative 23; Mismatches 52; Indels 19; Gaps 6;

Qy 15 SGAAALILICVTK-----AREGSEEDLDLEHMFRLPFSITMKRDPPTAQQFOEELKFKQ 69
 Db 160 SRTRLALITCNEEDSDIPRTGAEVDITGWTMLQNGSVYKKNLTASDMTELEAFA 219
 Qy 70 QAIDSRDPVSCAFVYIMAHG-REGFLKSGEDGMV-----KLENI,FEALNNKNCQALRAKP 124
 Db 220 HREPHKTS--DSTFLVFMHSHGIRREGICGKHSQVDPDIQLNMFNMLTKNCPSLKDKP 277
 Qy 125 KYVITIQACRGEQDPG-----ETVG 144
 Db 278 KVIITIQACRGD--SPGVWFKDSVG 300

RESULT 10
 C56084
 interleukin-1beta converting enzyme delta isozyme - human
 C:Species: Homo sapiens (man)
 C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Nov-1999
 C:Accession: C56084
 R:Alnemri, E.S.; Fernandes-Alnemri, T.; Litwack, G.
 J. Biol. Chem. 270, 4312-4317, 1995
 A>Title: Cloning and expression of four novel isoforms of human interleukin-1beta conv
 A:Reference number: A56084; MUID:95181414; PMID:7876192
 A:Accession: C56084
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-263 <ALN>
 A:Cross-references: GB:U13699; NID:9717043; PIDN:AAC50109.1; PID:9717044

D5 65 EIMELMDSVKEDHSKRSSFVC--VILSHGDEGVIFGTNGP-VDLKLTSPFRGDYCR 120

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D5 65 EIMELMDSVKEDHSKRSSFVC--VILSHGDEGVIFGTNGP-VDLKLTSPFRGDYCR 120

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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:40:11 ; Search time 7.23967 Seconds

(without alignments)
1050.081 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146

Perfect score: 752
Sequence: 1 MSNPRLEEKYDMSGALA.....YIQACRGQRDPGETVGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	747	99.3	242	1	ICB2_HUMAN
2	586	77.9	257	1	ICB2_MOUSE
3	222	29.5	424	1	ICB2_CHICK
4	210	27.9	435	1	ICB2_HUMAN
5	207	27.5	435	1	ICB2_MOUSE
6	205	27.3	312	1	ICB2_RAT
7	187.5	24.9	404	1	ICB2_HUMAN
8	184	24.5	404	1	ICB2_CANEA
9	180.5	24.0	405	1	ICB2_HORSE
10	180.5	24.0	480	1	ICB2_MOUSE
11	179.5	23.9	277	1	ICB3_HUMAN
12	178	23.7	366	1	ICB3_XENTIA
13	176	23.4	402	1	ICB3_RAT
14	175.5	23.3	382	1	ICB3_XENTIA
15	175.5	23.3	410	1	ICB3_FELICA
16	175	23.3	339	1	ICB3_DROME
17	175	23.3	404	1	ICB3_PIG
18	175	23.3	418	1	ICB3_HUMAN
19	173	23.0	402	1	ICB3_MOUSE
20	172.5	22.9	277	1	ICB3_RAT
21	169	22.5	303	1	ICB7_MOUSE
22	169	22.5	419	1	ICB3_MOUSE
23	169	22.5	479	1	ICB8_HUMAN
24	168	22.3	303	1	ICB7_MESAU
25	168	22.3	377	1	ICB4_HUMAN
26	167	22.2	416	1	ICB9_HUMAN
27	166	22.1	303	1	ICB7_HUMAN
28	165.5	22.0	277	1	ICB3_CRILLO
29	165	21.9	373	1	ICB4_HUMAN
30	163	21.7	377	1	ICB2_BOVIN
31	162.5	21.6	277	1	ICB3_MOUSE
32	153	20.3	276	1	ICB6_MOUSE
33	153	20.3	299	1	ICB1_SPOER

34	151.5	20.1	521	1	ICB4_HUMAN	Q92851 homo sapien
35	151	20.1	323	1	ICB1_DROME	O02002 drosophila
36	151	20.1	503	1	ICB3_DROME	P45573 caenorhabdi
37	145.5	19.3	496	1	ICB3_CAEUT	P45436 caenorhabdi
38	138	18.4	293	1	ICB6_HUMAN	P55212 homo sapien
39	136.5	18.2	282	1	ICB3_XENTIA	P55866 xenopus lae
40	84.5	11.2	520	1	ICB3_AQUAE	O06834 aquilifex aeo
41	82.5	11.0	167	1	ICB3_GALUS	O08814 galdiera s
42	82	10.9	484	1	ICB4_MOUSE	O35732 m caspi and
43	79.5	10.6	2779	1	LVA_DROME	O08651 drosophila
44	79	10.5	480	1	ICB4_HUMAN	O15519 h caspi and
45	79	10.5	510	1	ERS3_CERAE	Q9TU32 ceratophhec

ALIGNMENTS

RESULT 1
ICB2_HUMAN
ID ICB2_HUMAN STANDARD; PRT; 242 AA.
AC P31944; O95823;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
GN CASP14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22168928; PubMed=12181750;
RA Pistrillo G., Jost M., Srinivasula S.M., Baffa R., Poyet J.-L.,
RA Kari C., Lazebnik Y., Rodeck U., Alnemri E.S.;
RT "Expression and transcriptional regulation of caspase-14 in simple
RT and complex epithelia."
RL Cell Death Differ. 9:995-1006(2002).
RN [2]
RP SEQUENCE OF 68-74; 137-147 AND 154-162.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes."
RL Electrophoresis 13:960-969(1992).
CC -!- FUNCTION: May be involved in the death receptor and granzyme B
CC apoptotic pathways. May function as a downstream signal transducer
CC of cell death.
CC -!- SUBUNIT: May dimerize with large prodomain caspases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC
CC -----
CC EMBL; AF097874; AAD16173.1; -
CC PIR; JC7517; JC7517.
CC HSSP; P29466; IICE.
CC Aarhus/Ghent-2DPAGE; 6109; IEF.
CC MEROPS; C14.018; -
CC Genew; HGNC:1502; CASP14.
CC MIM; 605848; -
CC GO; GO:0004199; F:caspase activity; TAS.
CC GO; GO:0008544; P:epidermal differentiation; TAS.
CC InterPro; IPR002138; ICE_p10.

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DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase C14.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Apoptosis; Zymogen.
FT CHAIN 1 2
FT CHAIN 1 2
FT CHAIN 1 2
FT ACT_SITE 147 242 CASPASE-14 SUBUNIT 1 (POTENTIAL).
FT ACT_SITE 89 89 BY SIMILARITY.
FT ACT_SITE 132 132 BY SIMILARITY.
SQ SEQUENCE 242 AA; 27679 MW; E539FE78DD808A2 CRC64;

Query Match 99.3%; Score 747; DB 1; Length 242;
Best Local Similarity 99.3%; Pred. No. 4.5e-61;
Matches 145; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALHEMRQLEFESTMKRDPTAAQ 60
DB 1 MSNPRSLSEEEKYDMSGARLILCVTKARSGSEEDLDALHEMRQLEFESTMKRDPTAAQ 60
QY 61 FOELEKFOQALIDREDPVSCAFVLMAGHREGLKGEDEGMVLENTLEALNNKNCAL 120
DB 61 FOELEKFOQALIDREDPVSCAFVLMAGHREGLKGEDEGMVLENTLEALNNKNCAL 120
QY 121 RAKPKVYIIQACRGEQDPEGTVGSD 146
DB 121 RAKPKVYIIQACRGEQDPEGTVGSD 146
DB 121 RAKPKVYIIQACRGEQDPEGTVGSD 146

RESULT 2
ICER MOUSE STANDARD; PRT; 257 AA.
AC 089094;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DB Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (Mini-ICE) (MICE).
GN CASP14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SOURCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=C57BL/6J;
RX MEDLINE=99040667; PubMed=9823333;
RA Ahmed M., Srinivasula S.M., Hegde R., Mukattash R.,
RA Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification and characterization of murine caspase-14, a new
RT member of the caspase family.";
RL Cancer Res. 58:5201-5205(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Embryo;
RX MEDLINE=99222069; PubMed=10203698;
RA Van de Craen M., Van loo G., Pye S., Van Griekinge W.,
RA Van den brande I., Wollemans F., Fiers W., Declercq W.,
RA Vandenabeele P.;
RT "Identification of a new caspase homologue: caspase-14.";
RL Cell Death Differ. 5:838-846(1998).
RN [3]
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.
RX MEDLINE=99009076; PubMed=9792675;
RA Hu S., Snipas S.U., Vincenz C., Salvesen G., Dixit V.M.;
RT "Caspase-14 is a novel developmentally regulated protease.";
RL J. Biol. Chem. 273:29648-29653(1998)
DB -1- FUNCTION: Seems to be involved in the death receptor and granzyme
DB B apoptotic pathways. May function as a downstream signal

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CC transducer of cell death. May play a role in ontogenesis and skin
CC physiology.
CC -1- SUBUNIT: May dimerize with large prodomain caspases.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -1- TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain
CC and kidney.
CC -1- PM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROTEASE.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC
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CC
DR EMBL; AF092997; AAC63364.1; -.
DR EMBL; AJ007750; CAA07678.1; -.
DR HSBP; P29466; ILICE.
DR MEROPS; C14.018; -.
DR MGP; MGI:1335092; Casp14.
DR GO; GO:0006917; P:induction of apoptosis; IDA.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00656; Peptidase C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE; PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 7
FT CHAIN 8 257 CASPASE-14 SUBUNIT P18 (POTENTIAL).
FT CHAIN 93 93 CASPASE-14 SUBUNIT P11 (POTENTIAL).
FT ACT_SITE 93 93 BY SIMILARITY.
FT ACT_SITE 136 136 BY SIMILARITY.
FT MUTAGEN C-2A: DECREASE IN DEATH-INDUCING
FT ACTIVITY.
SQ SEQUENCE 257 AA; 29458 MW; A228D86DFBA0EB84 CRC64;

Query Match 77.9%; Score 586; DB 1; Length 257;
Best Local Similarity 76.0%; Pred. No. 2.3e-46;
Matches 111; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSNPRSLSEEEKYDMSGALALILCVTKARSGSEEDLDALHEMRQLEFESTMKRDPTAAQ 60
DB 5 MDDPQLQERYDMSGARLILCVTKARSGSEEDLDALHEMRQLEFESTMKRDPTAAQ 64
QY 61 FOELEKFOQALIDREDPVSCAFVLMAGHREGLKGEDEGMVLENTLEALNNKNCAL 120
DB 65 FLEELDFQQTIDNMEFPVSCAFVLMAGHREGLKGEDEGMVLENTLEALNNKNCAL 124
QY 121 RAKPKVYIIQACRGEQDPEGTVGSD 146
DB 125 RAKPKVYIIQACRGEQDPEGTVGSD 150

RESULT 3
ICER CHICK STANDARD; PRT; 424 AA.
AC 098943;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
DB 1L/1S).
GN CASP2 OR ICH1.

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OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).
 RC STRAIN=White leghorn; TISSUE=ovarian granulosa;
 RA MEDLINE=97368127; PubMed=9224894;
 RT Johnson A.L., Bridgman J.T., Bergeron L., Yuan J.;
 RT "Characterization of the avian ICH-1 cDNA and expression of ICH-1L
 RT mRNA in the hen ovary."
 RL Gene 192:227-233(1997).
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Might function by either
 CC activating some proteins required for cell death or inactivating
 CC proteins necessary for cell survival (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=ICH-1L;
 CC IsoId=Q98943-1; Sequence=Displayed;
 CC Note=Only form found in the ovary;
 CC Name=ICH-1S;
 CC IsoId=Q98943-2; Sequence=VSP_000803; VSP_000804;
 CC -1- PTM: Heterodimer of a small and a large subunit (By similarity).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 1 CARD domain.
 CC -----
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 CC -----
 CC EMBL; U64963; AAC29881.1; AUT_INIT.
 CC HSSP; P42574; ICP3.
 DR MEROPS; C14.006; -;
 DR InterPro: IPR001315; CARD.
 DR InterPro: IPR002138; ICE_P10.
 DR InterPro: IPR001309; ICE_P20.
 DR InterPro: IPR002398; Peptidase_C14.
 DR Pfam: PF00619; CARD; 1.
 DR Pfam: PF00656; Peptidase_C14; 1.
 DR PRINTS; PRO0376; ILIBENZIME.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PSS0209; CARD; 1.
 DR PROSITE; PSS0112; CASPASE_CYS; 1.
 DR PROSITE; PSS0112; CASPASE_HIS; 1.
 DR PROSITE; PSS0207; CASPASE_P10; 1.
 DR PROSITE; PSS0208; CASPASE_P20; 1.
 DR HydroLase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
 KW PROPEP 1 140
 FT CHAIN 141 308 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
 FT CHAIN 309 424 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
 FT CHAIN 315 424 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
 FT DOMAIN 7 96 CARD.
 FT ACT_SITE 248 248 BY SIMILARITY.
 FT ACT_SITE 291 291 BY SIMILARITY.
 FT VARSPIC 1 7 Missing (in isoform ICH-1S).
 FT VARSPIC 294 424 /FTId=VSP_000803.
 FT VARSPIC 294 424 DETROGDORDKERSDPGCEESDANKENILKILPTSRD
 FT MICGVACIKGTAMRNKTRGSMYIEALITTVAFSDSDTHVA
 FT DMLVKNRQIKQKRGYAPGTFRHCKKMSKSTLCIDIVY
 FT PEGYVPEK -> GVSGLHILPLPCCHCTCSNRQISEMI
 FT REMAKNGQIPQAVRWQTRKISSVCVCIAP1 (in
 FT isoform ICH-1S).
 FT /FTId=VSP_000804.
 FT SEQUENCE 424 AA; 47959 MW; 792810508B82F60 CRC64;
 Query Match 29.5%; Score 222; DB 1; Length 424;

Best Local Similarity 35.1%; Pred. No. 6,3e-13;
 Matches 52; Conservative 29; Mismatches 45; Indels 22; Gaps 4;
 QY 1 MSNFRSLSEKXYMSGALAILLC-----YTKAREGSEEDLDALHMRPROLPSTM 52
 DB 166 ISEPR-----GLAILLSNIHFSSSEKLEYRSGGVDCASLELFKHYGYTV 213
 QY 53 KRDPATQFOFELKFOQAIISREDPVSCAFVIMAHGREGLFGEDGEMVKTLENTPEAL 112
 DB 214 PHDSAEEMESALERFSKLP-HQDVDSCLVALISHVEGSGYGTGCKILLQLOEAFRLF 271
 QY 113 NNKNQALRAKPKXYIIQACRGQRDPG 140
 DB 272 DNANCPNQNKKPKFFLQACGDETRG 299
 RESULT 4
 ICE2 HUMAN STANDARD; PRT; 435 AA.
 AC P42575; P42576;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-1L/1S).
 GN CASP2 OR ICH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Fetal brain;
 RX MEDLINE=94373811; PubMed=8087842;
 RA Wang L., Mura M., Bergeron L., Zhu H., Yuan J.;
 RT "Ich-1, an Ice/Ced-3-related gene, encodes both positive and negative
 RT regulators of programmed cell death."
 RL Cell 78:739-750(1994).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS LEU-155; ALA-161 AND
 RP GLY-424.
 RA Rieder M.J., Livingston R.U., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Wiltrak L.A., Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Doeber A., Martinka S., Maupin R.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP CLEAVAGE SITES.
 RX MEDLINE=96206041; PubMed=8654923;
 RA Xue D., Shaham S., Horvitz H.R.;
 RT "The Caenorhabditis elegans cell-death protein CED-3 is a cysteine
 RT protease with substrate specificities similar to those of the human
 RT CPP32 protease."
 RL Genes Dev. 10:1073-1083(1996).
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Might function by either
 CC activating some proteins required for cell death or inactivating
 CC proteins necessary for cell survival.
 CC -1- SUBUNIT: Heterodimer of a small and a large subunit (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Isoforms differ in the N- and C-termini;
 CC Name=ICH-1L;
 CC IsoId=P42575-1; Sequence=Displayed;
 CC Note=Acts as a positive regulator of apoptosis;
 CC Name=ICH-1S;
 CC IsoId=P42575-2; Sequence=VSP_000801; VSP_000802;
 CC Note=Acts as a negative regulator of apoptosis;
 CC -1- TISSUE SPECIFICITY: Expressed in larger amounts in the embryonic

CC lung, liver and kidney than in the heart and brain. In the adults
 CC higher level expression is seen in the placenta, lung, kidney,
 CC pancreas than in the heart, brain, liver and skeletal muscle.
 CC -1- PTH: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
 CC THAT OF OTHER CASPASES.
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 1 CARD domain.
 CC -----
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 CC EMBL; U13021; AAA58959.1; -
 CC EMBL; U13022; AAA58960.1; -
 CC EMBL; AY219042; AA025653.1; -
 CC EMBL; AC073342; AAP22346.1; -
 CC PIR; A54821; A54821.
 CC HSP; P23466; IICE.
 CC MEROPS; C14.006; -
 CC Genew; HGNC:1503; CASP2.
 CC MIM; 600639; -
 CC GO; GO:0004202; F:caspase-2 activity; TAS.
 CC GO; GO:0019899; F:enzyme binding; ISS.
 CC GO; GO:0008632; P:apoptotic program; TAS.
 CC GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 CC InterPro; IPR002138; CARD.
 CC InterPro; IPR001309; ICE_p10.
 CC InterPro; IPR002398; Peptidase_C14.
 CC Pfam; PF006619; CARD; 1.
 CC Pfam; PF00656; Peptidase_C14; 1.
 CC PRINTS; PR00376; ILIBCENTZME.
 CC SMART; SM00114; CARD; 1.
 CC SMART; SM00115; CASC; 1.
 CC PROSITE; PS50209; CARD; 1.
 CC PROSITE; PS01122; CASPASE_CYS; 1.
 CC PROSITE; PS01121; CASPASE_HIS; 1.
 CC PROSITE; PS50207; CASPASE_P10; 1.
 CC PROSITE; PS50208; CASPASE_P20; 1.
 CC HydroLase; Thiol protease; Apoptosis; Zymogen; Polymorphism;
 CC Alternative splicing.
 CC FT PROPEP 1 152
 FT CHAIN 153 308 CASPASE-2 SUBUNIT P18.
 FT PROPEP 309 316
 FT CHAIN 317 435 CASPASE-2 SUBUNIT P13.
 FT CHAIN 331 435 CASPASE-2 SUBUNIT P12.
 FT DOMAIN 15 103 CARD.
 FT ACT_SITE 260 260 BY SIMILARITY.
 FT ACT_SITE 303 303 BY SIMILARITY.
 FT VARSPIC 1 14 Missing (in isoform ICH-1S).
 FT VARSPIC 306 435 /FTID=VSP_000801.
 FT VARSPIC 306 435 DETRGVDQDDGNHAGSPGCESDAGKEKLPRLPRTSD
 FT VARSPIC 306 435 MIVGACIKGTAMRTKGSWYIEALAVFSPRACDMHYA
 FT VARSPIC 306 435 DMIVKVALIKDREGVAPGTFPHRCKMEKSEVSTICRHHYL
 FT VARSPIC 306 435 PFGHPT -> GGAGISLHLLFTATATSLAL (in
 FT VARSPIC 306 435 isoform ICH-1S).
 FT VARSPIC 306 435 /FTID=VSP_000802.
 FT VARSPIC 306 435 V -> L.
 FT VARSPIC 306 435 /FTID=VAR_016334.
 FT VARSPIC 306 435 P -> A.
 FT VARSPIC 306 435 /FTID=VAR_016335.
 FT VARSPIC 306 435 R -> G.
 FT VARSPIC 306 435 /FTID=VAR_016336.
 FT VARSPIC 306 435 C -> S: LOSS OF FUNCTION.
 FT VARSPIC 306 435 A -> T: LOSS OF FUNCTION.
 FT VARSPIC 306 435 MUTAGEN 303 303 /FTID=VAR_016336.
 FT VARSPIC 306 435 MUTAGEN 352 352 C -> S: LOSS OF FUNCTION.
 FT VARSPIC 306 435 SEQUENCE 435 AA; 48855 MW; 1652EC73F6286FB7 CRC64;
 Query Match 27.9%; Score 210; DB 1; Length 435;
 Best Local Similarity 37.5%; Fred. No. 8.1e-12;

Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;
 QY 29 REGSEEDLDAEHMFROLPFESTMWRDPTAPOFEBELFOQALDSRRDPVSCAFVYMA 88
 DB 202 RSGGDVHSTLVTLVFKLLGVYVHVCDDTAQEMQKUNFAQ-IPAHRYVDSQ-IVALLS 259
 QY 89 HGRGFLKGEDEWVKLENLFALNNKCAIRAKPKYVYIQAQRGEQDRDP 140
 DB 260 HGVEGAIYGVDKLLQLEVFQLPDMNCPSTLQKKPKMFIAQCRGDETDG 311
 RESULT 5
 ICE2 MOUSE
 ID ICE2 MOUSE STANDARD; PRT; 435 AA.
 AC P29594; 008737;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 15-MAR-2004 (Rel. 43, last annotation update)
 DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2
 DE protein).
 GN CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=95047319; PubMed=7958843;
 RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
 RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
 RT protein similar to the product of the Caenorhabditis elegans cell
 RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
 RL Genes Dev. 8:1613-1626 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/An;
 RX MEDLINE=97190206; PubMed=9039361;
 RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,
 RA van Ioo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
 RA Fiers W.;
 RT "Characterization of seven murine caspase family members.";
 RL FEBS Lett. 403:61-69 (1997).
 RN [3]
 RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92328780; PubMed=1378265;
 RA Kumar S., Tomooka Y., Noda M.;
 RT "Identification of a set of genes with developmentally down-regulated
 RT expression in the mouse brain.";
 RL Biochem. Biophys. Res. Commun. 185:1155-1161 (1992).
 CC -1- FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. Might function by either
 CC activating some proteins required for cell death or inactivating
 CC proteins necessary for cell survival. May be important in
 CC multistep carcinogenesis.
 CC -1- SUBUNIT: Heterodimer of a small and a large subunit (by
 CC similarity).
 CC -1- TISSUE SPECIFICITY: High level expression seen in the embryonic
 CC CNS, liver, lung, kidney, small intestine, and hair follicles of
 CC skeletal muscle, submandibular gland and thymus. In the adult, it
 CC is highly expressed in spleen, lung and kidney. Moderately in the
 CC brain, heart, testis, liver. Low levels in the thymus, skeletal
 CC muscle, ovary and gut.
 CC -1- DEVELOPMENTAL STAGE: During embryonic development is highly
 CC expressed in several types of mouse tissue undergoing high rates
 CC of programmed cell death such as central nervous system and
 CC kidney.
 CC -1- PTH: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
 CC THAT OF OTHER CASPASES (BY SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 1 CARD domain.

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CC -----
DR EMBL: D28492; BAA25876.1; ALT INIT.
DR EMBL: Y13085; CAA73527.1; ALT_INIT.
DR HSSP: P42574; IC93.
DR MEROPS: C14.006; -.
DR MGD: MGI:97295; Casp2.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PRO0376; ILBENZYM.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR KX: Hydrolyase; Thiol protease; Apoptosis; Zymogen.
DR PROPEP: 152.
DR CHAIN: 153 316 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
DR CHAIN: 317 435 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
DR CHAIN: 331 435 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
DR DOMAIN: 15 103 CARD.
DR ACT_SITE: 260 260 BY SIMILARITY.
DR ACT_SITE: 303 303 C->G: LOSS OF FUNCTION.
DR MUTAGEN: 303 303 MISSING (IN REF. 1).
DR CONFLICT: 71 71
SQ SEQUENCE 435 AA; 48896 MW; 8984E6AA7676A676 CRC64;

Query Match 27.5%; Score 207; DB 1; Length 435;
Best Local Similarity 37.5%; Pred. No. 1.5e-11;
Matches 42; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHEMFROLPESTMKRDPFAEQFOEELKEFOALDSREDFVSCAFVYMA 89
DB 202 RSGGDVDTHTLVTLFKLGNVHLYDQTAQEMQEKLNPAQ-LPAHRTDSCV-VALLS 259

QY 89 HGRBGLKGDGEMVKLENTFEALNNKNCQALPAKPKVYIIQAQGRGQDPG 140
DB 260 HGEVGGIYVDKLLQLQEVFRLEFDNANCPSLQNKPKMFIQAQCRGDETRG 311

RESULT 6
ICB2 RAT STANDARD; PRT; 312 AA.
ID ICB2 RAT
AC P55215; O35398;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (ICB-1 protease)
DE (Fragment).
DE CASP2 OR ICH1.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RS SEQUENCE OF 1-257 FROM N.A.
RC TISSUE=Kidney cortex;
RX MEDLINE=96191309; PubMed=9530276;
RA Kaushal G.P., Singh A.B., Shah S.V.;
RT "Identification of gene family of caspases in rat kidney and altered

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RT expression in ischemia-reperfusion injury.";
RN Am. J. Physiol. 274:F587-F595(1998).
RN [2]
RN SEQUENCE OF 131-312 FROM N.A.
RP TISSUE=Ovary;
RC MEDLINE=96042508; PubMed=7588240;
RX MEDLINE=96042508; PubMed=7588240;
RA Hirschfeld A.N., Tilly J.L.;
RA Hirschfeld A.N., Tilly J.L.;
RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
RT endonuclease activity from morphological apoptosis in granulosa cells
RT of the ovarian follicle.";
RL Endocrinology 136:5042-5053(1995).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival (By similarity).
CC -1- SUBUNIT: Heterodimer of a small and a large subunit (By
CC similarity).
CC -1- PTM: THE MATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
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CC -----
DR EMBL: AF025671; AAB82567.1; -.
DR EMBL: U34684; AAC52260.1; -.
DR PIR: I67436; I67436.
DR HSP: P29466; 1ICE.
DR MEROPS: C14.006; -.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001309; ICE_P20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PRO0376; ILBENZYM.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR PROSITE: PS01122; CASPASE_HIS; 1.
DR PROSITE: PS01121; CASPASE_P10; 1.
DR Hydrolyase; Thiol protease; Apoptosis; Zymogen.
DR NON_TER: 1
FT CHAIN: <1 266 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
FT CHAIN: 267 >312 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
FT CHAIN: 281 >312 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
FT DOMAIN: <1 55 CARD.
FT ACT_SITE: 210 210 BY SIMILARITY.
FT ACT_SITE: 253 253 BY SIMILARITY.
FT NON_TER: 312 312
SQ SEQUENCE 312 AA; 35070 MW; 318A0746212E9646 CRC64;

Query Match 27.3%; Score 205; DB 1; Length 312;
Best Local Similarity 37.5%; Pred. No. 1.6e-11;
Matches 42; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHEMFROLPESTMKRDPFAEQFOEELKEFOALDSREDFVSCAFVYMA 89
DB 152 RSGGDVDTHTLVTLFKLGNVHLYDQTAQEMQEKLNPAQ-LPAHRTDSCV-VALLS 209

QY 89 HGRBGLKGDGEMVKLENTFEALNNKNCQALPAKPKVYIIQAQGRGQDPG 140
DB 210 HGEVGGIYVDKLLQLQEVFRLEFDNANCPSLQNKPKMFIQAQCRGDETRG 261

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RESULT 7
IL1BC_HUMAN
ID IL1BC_HUMAN STANDARD; PRT; 404 AA.
AC P29466;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Interleukin-1 beta converting enzyme precursor (IL-1BC) (EC 3.4.22.36) (IL-1
DE beta converting enzyme) (ICE) (Interleukin-1 beta converting enzyme)
DE (P45) (Caspase-1) (CASP-1).
GN CASP1 OR IL1BC OR IL1BCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND ACTIVE SITE.
RX MEDLINE=92244338; PubMed=1574116;
RA Thornberry N.A., Bull H.G., Calaycay J.R., Chapman K.T., Howard A.D.,
RA Kostura M.J., Miller D.K., Molinieux S.M., Weidner J.R., Annins U.,
RA Elliston K.O., Ayala J.M., Casano F.J., Chin J., Ding G.J., F.,
RA Egger L.A., Gaffney E.P., Limjoco G., Palyna O.C., Raju M.,
RA Rolando A.M., Salley J.P., Yamin T.-T., Lee T.D., Shively J.E.,
RA McCross M., Mumford R.A., Schmidt J.A., Tocci M.J.,
RT "A novel heterodimeric cysteine protease is required for
RT interleukin-1 beta processing in monocytes."
RL Nature 356:768-774 (1992).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 120-142.
RX MEDLINE=92229430; PubMed=1373520;
RA Corretti D.P., Kozlosky C.J., Mosley B., Nelson N., Van Ness K.,
RA Greenstreet T.A., March C.J., Kronheim S.R., Druck T.,
RA Camarazaro L.A., Huebner K., Black R.A.,
RT "Molecular cloning of the interleukin-1 beta converting enzyme."
RL Science 256:97-100 (1992).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94320145; PubMed=8044845;
RA Walker N.P.C., Talianian R.V., Brady K.D., Dang L.C., Bump N.J.,
RA Ferenz C.R., Franklin S., Ghayur T., Hackett M.C., Hamill L.D.,
RA Herzog L., Huganir M., Houy W., Markovich J.A., McGinness L.,
RA Olewicz E., Paskind M., Pratt C.A., Reis P., Summari A.,
RA Terranova M., Welch J.P., Xiong L., Moeller A., Tracey D.E., Kamen R.,
RA Wong W.W.,
RT "Crystal structure of the cysteine protease interleukin-1 beta-
RT converting enzyme: a (p20/p10)2 homodimer."
RL Cell 78:343-352 (1994).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.73 ANGSTROMS).
RX MEDLINE=97199458; PubMed=9190283;
RA Rano T.A., Timkey T., Peterson E.P., Rotonda J., Nicholson D.W.,
RA Becker J.W., Chapman K.T., Thornberry N.A.,
RT "A combinatorial approach for determining protease specificities:
RT application to interleukin-1beta converting enzyme (ICE)."
RL Chem. Biol. 4:149-155 (1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=99142310; PubMed=9987822;
RA Okamoto Y., Anan H., Nakai E., Morihira K., Yonetoku Y., Kurihara H.,
RA Sakashita H., Terai Y., Takeuchi M., Shibamura T., Isonura Y.,
RT "Peptide based interleukin-1 beta converting enzyme (ICE) inhibitors:
RT synthesis, structure activity relationships and crystallographic
RT study of the ICE-inhibitor complex."
RL Chem. Pharm. Bull. 47:11-21 (1999).
RN [6]
RP ALTERNATIVE SPLICING, AND FUNCTION.
RX MEDLINE=95181414; PubMed=7876192;
RA Alnemri E.S., Fernandes-Alnemri T., Litwack G.,
RT "Cloning and expression of four novel isoforms of human interleukin-1
RT beta converting enzyme with different apoptotic activities."
RL J. Biol. Chem. 270:4312-4317 (1995).
CC -!- FUNCTION: Thiol protease that cleaves IL-1 beta between an Asp and
CC an Ala, releasing the mature cytokine which is involved in a

CC variety of inflammatory processes. Specifically inhibited by the
CC compox virus Crma protein.
CC -!- CATALYTIC ACTIVITY: Release of interleukin 1-beta by specific
CC cleavage at 116-Asp|-Ala-117 and 27-Asp|-Gly-28 bonds in
CC precursor. Also hydrolyzes the small-molecule substrate, Ac-Tyr-
CC Val-Ala-Asp|-NHMeC.
CC -!- SUBUNIT: Tetramer that consists of two heterodimers of a 20 kDa
CC (p20) and a 10 kDa (p10) subunits. The p20 subunit can also form a
CC heterodimer with the epsilon isoform which then has an inhibitory
CC effect.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=5;
CC Comment=Additional isoforms seem to exist;
CC Name=Alpha;
CC IsoId=P29466-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P29466-2; Sequence=VSP_000798;
CC Name=Gamma;
CC IsoId=P29466-3; Sequence=VSP_000799;
CC Name=Delta;
CC IsoId=P29466-4; Sequence=VSP_000799, VSP_000800;
CC Note=Apoptosis inactive;
CC Name=Epsilon;
CC IsoId=P29466-5; Sequence=VSP_000797;
CC Note=Apoptosis inactive;
CC -!- TISSUE SPECIFICITY: Expressed in larger amounts in spleen and
CC lung. Also found in liver, heart, skeletal muscle, kidney and
CC testis. No expression in the brain.
CC -!- PTM: The two subunits are derived from the precursor sequence by
CC an autocatalytic mechanism.
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -!- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC -----
CC EMBL: X65019; CAA46153.1; -
CC EMBL: M87507; AAA66942.1; -
CC EMBL: U13697; AAC50107.1; -
CC EMBL: U13698; AAC50108.1; -
CC EMBL: U13699; AAC50109.1; -
CC EMBL: U13700; AAC50110.1; -
CC PIR: A54263; A42677.
CC PIR: A56084; A56084.
CC PIR: B56084; B56084.
CC PIR: C56084; C56084.
CC PIR: D56084; D56084.
CC PDB: 1ICE; 28-JUL-95.
CC PDB: 1IBC; 11-FEB-98.
CC PDB: 1BMQ; 29-JUL-98.
CC MEROPS: C14.001; -
CC Genew: HGNC:1495; CASP1.
CC MIM: 147678; -
CC GO: GO:0008656; F: caspase activator activity; TAS.
CC GO: GO:0004201; F: caspase-1 activity; TAS.
CC GO: GO:0006915; P: apoptosis; TAS.
CC GO: GO:0009405; P: pathogenesis; TAS.
CC GO: GO:0006508; P: proteolysis and peptidolysis; TAS.
CC GO: GO:0007165; P: signal transduction; TAS.
CC InterPro: IPR001315; CARD.
CC InterPro: IPR002138; ICE p10.
CC InterPro: IPR001309; ICE p20.
CC InterPro: IPR002398; Peptidase_C14.
CC Pfam: PF00619; CARD; 1.
CC Pfam: PF00656; Peptidase_C14; 1.
CC PRINTS: PR00376; IL1BCENZYM.
CC SMART: SMO0114; CARD; 1.

DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR Hydrolyase; Thiol protease; Zymogen; 3D-structure;
 KM Alternative splicing.
 FT PROPEP 1 119
 FT CHAIN 120 297 INTERLEUKIN-1 BETA CONVERTASE P20.
 FT PROPEP 298 316
 FT CHAIN 317 404 INTERLEUKIN-1 BETA CONVERTASE P10.
 FT DOMAIN 1 91 CARD.
 FT ACT_SITE 237 237
 FT ACT_SITE 285 285
 FT VARSPPLIC 20 335 Missing (in isoform Epsilon).
 FT VARSPPLIC 92 112 /FTId=VSP_000797.
 FT VARSPPLIC 20 112 Missing (in isoform Beta).
 FT VARSPPLIC 20 112 /FTId=VSP_000798.
 FT VARSPPLIC 20 112 Missing (in isoform Gamma and isoform Delta).
 FT VARSPPLIC 288 335 /FTId=VSP_000799.
 FT VARSPPLIC 288 335 Missing (in isoform Delta).
 FT VARSPPLIC 288 335 /FTId=VSP_000800.
 FT HELIX 138 148
 FT HELIX 149 151
 FT STRAND 152 152
 FT TURN 158 160
 FT STRAND 164 169
 FT TURN 180 181
 FT HELIX 182 196
 FT TURN 197 197
 FT STRAND 199 204
 FT HELIX 208 220
 FT HELIX 222 226
 FT STRAND 230 235
 FT STRAND 238 238
 FT STRAND 242 244
 FT TURN 246 247
 FT STRAND 255 257
 FT HELIX 258 265
 FT TURN 267 269
 FT HELIX 271 273
 FT TURN 274 275
 FT STRAND 278 283
 FT STRAND 289 289
 FT STRAND 327 331
 FT TURN 335 336
 FT STRAND 337 337
 FT STRAND 340 342
 FT HELIX 343 345
 FT STRAND 346 347
 FT HELIX 348 360
 FT TURN 361 363
 FT HELIX 366 375
 FT TURN 376 377

Query Match 24.9%; Score 187.5; DB 1; Length 404;
 Best Local Similarity 35.2%; Pred. No. 8.3e-10;
 Matches 51; Conservative 23; Mismatches 52; Indels 19; Gaps 6;

QY 15 SGAALALILCVTK-----AREGSEEDDALEHMRQLRFSTMKRDPFAQFOEELKFEQ 69
 DB 160 SRTRLALITNEEDDSIPRTGAVDITGMMLLQNGYSYDVAKNLTASDMTELEAFA 219
 QY 70 QALDSREDPVSCAFVITMAHG-RGFLKGEDEVY---KLENIPELANKKCAALAKP 124
 DB 220 HRFPHKTS--DSTFLVMSHGIRGICGKKSSEQVPIQLNALFNLMTNCPSLDKP 277
 QY 125 KVVYIIACRGGRQDPG-----ETVG 144
 DB 278 KVVIIQAKGD--SPGVVWFKDSVG 300

RESULT 8
 ID 11BC CANFA STANDARD; PRT; 404 AA.
 AC Q9MZV7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interleukin-1 beta converting enzyme (ICE) (Interleukin-1 beta converting enzyme)
 DE beta converting enzyme (ICE) (Interleukin-1 beta converting enzyme)
 DE (P45) (Caspase-1) (CASP-1).
 GN CASP1 OR IL1BC.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP MEDLINE=20284946; PubMed=10826695;
 RA Taylor S., Hanton L., McGillivray C., Gault E.A., Argyre D.J.,
 RA O'Leary D.E., Nicolson L.;
 RT "Cloning and sequencing of feline and canine ice-related cDNAs
 RT encoding hybrid caspase-1/caspase-13-like propeptides.";
 RL DNA Seq. 10:387-394(2000).
 CC -!- FUNCTION: Thiol protease that cleaves IL-1 beta between an Asp and
 CC an Ala, releasing the mature cytokine which is involved in a
 CC variety of inflammatory processes (By similarity).
 CC -!- CATALYTIC ACTIVITY: Release of interleukin 1-beta by specific
 CC cleavage at 116-Asp-[Ala-117 and 27-Asp-[Gly-28 bonds in
 CC precursor. Also hydrolyzes the small-molecule substrate, Ac-Tyr-
 CC Val-Ala-Asp-[NHMeC.
 CC -!- SUBUNIT: Tetramer that consists of two heterodimers of a 20 kDa
 CC (p20) and a 10 kDa (p10) subunits. The p20 subunit can also form a
 CC heterodimer with the epsilon isoform which then has an inhibitory
 CC effect (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the epsilon isoform which then has an inhibitory
 CC an autocatalytic mechanism
 CC -!- SIMILARITY: Belongs to peptidase family C14.
 CC -!- SIMILARITY: Contains 1 CARD domain.
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 CC -----
 DR EMBL; AF135967; AAF64388.1; -;
 DR HSSP; P29466; 1ICE.
 DR MEROPS; C14.024; -;
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; IL1BCENZME.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS50209; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 KW Hydrolyase; Thiol protease; Zymogen.
 FT PROPEP 1 119 POTENTIAL.
 FT CHAIN 120 297 INTERLEUKIN-1 BETA CONVERTASE P20.
 FT PROPEP 298 316 POTENTIAL.
 FT CHAIN 317 404 INTERLEUKIN-1 BETA CONVERTASE P10.
 FT DOMAIN 1 91 CARD.
 FT ACT_SITE 237 237 BY SIMILARITY.

FT ACT SITE 285 285 BY SIMILARITY.
SQ SEQUENCE 404 AA; 45662 MW; BCSA505CD7DBDFDD CRC64;
Query Match 24.5%; Score 184; DB 1; Length 404;
Best Local Similarity 33.8%; Pred. No. 1.7e-09;
Matches 46; Conservative 27; Mismatches 43; Indels 20; Gaps 5;
QY 19 LALLICVTK----AREGSEEDLDALHEMFRLRFEETMKRDPFAOEELFEKFOQAID 73
DB 164 LALLICNIEFDHSLTRDGAELDIAGMESILEGLGYSVVVKRLAKGMESVLRFPARPE 223
QY 74 SREDPVCAPVYMAHGRGFLKG-----EGGEVKLENLPEALNNKXQALRAKPK 125
DB 224 HKSS--DSTFLVMSH---GLINGICGTANSVENPDVLAVDITQIFNNRHLMKDKPK 278
QY 126 VYIIQACRGQRDPGE 141
DB 279 VTIIOACRGE--NGE 292
RESULT 9
IIBC HORSE
ID IIBC HORSE STANDARD; PRT; 405 AA.
AC 09TVL3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Interleukin-1 beta convertase precursor (IL-1BC) (EC 3.4.22.36) (IL-1 beta converting enzyme) (ICE) (Interleukin-1 beta converting enzyme) (P45) (Caspase-1) (CASP-1).
GN CASP1 OR IL1BC.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99304505; PubMed=10376217;
RA Wardlaw S., Penha-Goncalves M.N., Argyle D.J., Onions D.E., Nicolson L.;
RT "Nucleotide sequence of equine caspase-1 cDNA."
RL DNA Seq. 10:133-137(1999).
CC -1- FUNCTION: Thiol protease that cleaves IL-1 beta between an Asp and an Ala, releasing the mature cytokine which is involved in a variety of inflammatory processes (By similarity).
CC -1- CATALYTIC ACTIVITY: Release of interleukin-1-beta by specific cleavage at 116-Asp-Ala-117 and 27-Asp-Gly-28 bonds in Val-Ala-Asp-NHMeC
CC -1- SUBUNIT: Tetramer that consists of two heterodimers of a 20 kDa (p20) and a 10 kDa (p10) subunits. The p20 subunit can also form a heterodimer with the epsilon isoform which then has an inhibitory effect (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: The two subunits are derived from the precursor sequence by an autocatalytic mechanism.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
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CC EMBL; AF090119; AAD46400.1; --
DR HSSP; P29466; ICE.
DR MEROPS; C14.001; --
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.

DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS_1.
DR PROSITE; PS01121; CASPASE_HIS_1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; zymogen; Polymorphism.
FT PROPEP 1 119
FT CHAIN 120 298
FT PROPEP 299 317
FT CHAIN 318 405
FT DOMAIN 1 91
FT ACT SITE 238 238
FT ACT SITE 286 286
FT VARIANT 203 203
FT VARIANT 305 305
SQ SEQUENCE 405 AA; 45331 MW; 7CE8729B359CC17 CRC64;
Query Match 24.0%; Score 180.5; DB 1; Length 405;
Best Local Similarity 34.3%; Pred. No. 3.6e-09;
Matches 49; Conservative 24; Mismatches 53; Indels 17; Gaps 5;
QY 10 ERYDMGAA----LALLICVTK----AREGSEEDLDALHEMFRLRFEETMKRDPFAE 59
DB 151 EWPYIMKSWTRFRLALINTEFDNISRRAGAEVDIAKVKVLEGLGYSVEVXENITAL 210
QY 60 QFOEELFEKFOQALDSREDPVCAPVYMAHG-REGFLKSGDEMY---KLEMLFEALNN 114
DB 211 DMTTEKAPARPEHSS--DSTFLVMSHGIREIGCKKFSKVPDVLVENVTFQIFNT 268
QY 115 KNCQALRAKPKVYIIQACRGQR 137
DB 269 RNCPNLRDKPKVYIIQACRGENG 291
RESULT 10
ICE8 MOUSE
ID ICE8 MOUSE STANDARD; PRT; 480 AA.
AC 0891I0; O35669;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-8 precursor (EC 3.4.22.-).
GN CASP8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=129/SVJ.
RX MEDLINE=98316661; PubMed=9654089;
RA Sakamaki K., Tsukumo S.-I., Yonehara S.;
RT "Molecular cloning and characterization of mouse caspase-8."
RL Eur. J. Biochem. 253:399-405(1998).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=9057979; PubMed=9837723;
RX Van de Craen M., Van Loo G., Declercq W., Schotte P., Van den Brande I., Mandruzzato S., van der Bruggen P., Fiers W., Vandenbeele P.;
RT "Molecular cloning and identification of murine caspase-8."
RL J. Mol. Biol. 284:1017-1026(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N, TISSUE=Colon, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buehler K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stetleron M., Soares M.B., Bonaldo M.F., Cavaant T.L., Scheetz T.E.,
 RA Brownstein W.J., Usdin T.B., Toshiyuki S., Cantinot P., Prange C.,
 RA Rana S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shechenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RP SEQUENCE OF 57-476 FROM N.A.
 RA Kischkel P., Kischkel P., Poustka A., Krammer P.,
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Most upstream protease of the activation cascade of
 CC caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A
 CC induced cell death. Binding to the adapter molecule FADD recruits
 CC it to either receptor. The resulting aggregate called death-
 CC inducing signaling complex (DISC) performs CASP8 proteolytic
 CC activation. The active dimeric enzyme is then liberated from the
 CC DISC and free to activate downstream apoptotic proteases.
 CC Proteolytic fragments of the N-terminal propeptide (termed CAP3,
 CC CAP5 and CAP6) are likely retained in the DISC. Cleaves and
 CC activates CASP3, CASP4, CASP6, CASP7, CASP9 and CASP10. May
 CC participate in the G2M4 apoptotic pathways. Cleaves APOPT.
 CC Hydrolyzes the small-molecule substrate, Ac-Asp-Glu-Val-Asp-|-AMC.
 CC Likely target for the complex virus CRMA death inhibitory protein.
 CC -1- ENZYME REGULATION: Inhibited by Z-VAD-FK, Crma and P35.
 CC -1- SUBUNIT: Heterodimer of a 18 kDa (P18) and a 10 kDa (P10) subunit.
 CC Interacts with Fadd, Cflar and Peals (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in a wide variety of tissues.
 CC Highest expression in spleen, thymus, lung, liver and kidney.
 CC Lower expression in heart, brain, testis and skeletal muscle.
 CC -1- DEVELOPMENTAL STAGE: In the embryo, highest expression occurs at
 CC day 7.
 CC -1- PTM: Generation of the subunits requires association with the
 CC death-inducing signaling complex (DISC), whereas additional
 CC processing is likely due to the autocatalytic activity of the
 CC activated protease. GZMB and CASP10 can be involved in these
 CC processing events (By similarity).
 CC -1- SIMILARITY: Belongs to peptidase family C14.
 CC -1- SIMILARITY: Contains 2 death effector (DED) domains.
 CC -----
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 CC -----
 DR EMBL: AF067841; AAC40132.1; -
 DR EMBL: AF067835; AAC40132.1; JOINED.
 DR EMBL: AF067836; AAC40132.1; JOINED.
 DR EMBL: AF067837; AAC40132.1; JOINED.
 DR EMBL: AF067838; AAC40132.1; JOINED.
 DR EMBL: AF067839; AAC40132.1; JOINED.
 DR EMBL: AF067840; AAC40132.1; JOINED.
 DR EMBL: AF067834; AAC40131.1; -
 DR EMBL: AJ007749; CA007677.1; -
 DR EMBL: BC006737; AA067677.1; -
 DR EMBL: BC049955; AA049955.1; -
 DR EMBL: AJ000641; CA004136.1; -
 DR HSSP: Q15806; 10DU.

DR MEROPS; C14.009; -
 DR MED; MG1:1261423; Casp8.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0004205; F:caspase-8 activity; IDA.
 DR GO; GO:0006915; P:apoptosis; IDA.
 DR InterPro; IPR001875; DED.
 DR InterPro; IPR002138; ICE_P10.
 DR InterPro; IPR001309; ICE_P20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF01335; DED; 2.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; IL1BCENZYM.
 DR SMART; SM00031; DED; 2.
 DR SMART; SM00031; DED; 2.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS50207; CASPASE_P10; 1.
 DR PROSITE; PS50208; CASPASE_P20; 1.
 DR PROSITE; PS50168; DED; 2.
 KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Repeat.
 FT PROPEP 1 218
 FT CHAIN 219 376
 FT PROPEP 377 387
 FT CHAIN 388 480
 FT ACT_SITE 319 319
 FT ACT_SITE 362 362
 FT DOMAIN 3 80
 FT DOMAIN 101 177
 FT CONFLICT 68 71
 FT CONFLICT 94 99
 FT CONFLICT 96 96
 FT CONFLICT 103 107
 FT CONFLICT 475 475
 FT CONFLICT 475 475
 SQ SEQUENCE 480 AA; 55356 MW; 045268AB3DE5D4F CRC64;
 Query Match 24.0%; Score 180.5; DB 1; Length 480;
 Best Local Similarity 33.3%; Pred. No. 4.4e-09;
 Matches 38; Conservative 21; Mismatches 52; Indels 3; Gaps 1;
 QY 27 KAREGSEEDLDALHMFROIFRSTNKPDTAFQFOELHKKFOQAIDSBDPVSCAFVYL 86
 Db 260 KQKGGDCKCKEALSKTFKELHFRIVSYDCTANEIHIEILLEGYQASDHKKMD--CFICCI 316
 QY 87 MARGRGFLKGEHGVKLENLEFALNNKCCQALRAKPKVYIIQACRGEORDFG 140
 Db 317 LSHGDKGVVYGTGDKASGYDILSYFTGSKCPSLSGKPKLFIQACGGSNFKG 370
 RESULT 11
 ICES_HUMAN
 ID ICES_HUMAN STANDARD; PRT; 277 AA.
 AC P42574; Q96AN1; Q96KP2;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptin precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (SRBP cleavage activity 1)
 DE (SCA-1).
 GN CASP3 OR CPP32.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ON NCB1_TaxID=9606;
 RX NCB1_TaxID=9606;
 RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
 RC TISSUE=T-cell;
 RX MEDLINE=95074098; PubMed=7983002;
 RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
 RT "CPP32, a novel human apoptotic protein with homology to
 RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
 RT interleukin-1 beta-converting enzyme.";
 RT J. Biol. Chem. 269:30761-30764(1994).
 RL

[12] SEQUENCE FROM N.A.
RA MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beller D.R., Poirier G., Salvesen G.S., Dixit V.M.,
RA "Yama/CP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Vallette F.M., Oliver L.J.,
RT "Control of the activation of the procaspase-3 by a sequence located
RT at the N-terminus of the p17 subunit.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., McKerson D.A.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman G.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udén T.B., Tostolyuk S., Carinici P., Prange C.,
RA Raba S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mulaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grzymala J., Schmutz J., Myers R.M.,
RA Buterfield A.C., Krzywinski M.I., Skalska U., Smolins D.E.,
RA Scherach A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 29-46 AND 175-193, AND FUNCTION.
RX MEDLINE=95319529; PubMed=7596430;
RA Nicholson D.W., Ali A., Thornberry N.A., Vailancourt J.P., Ding C.K.,
RA Gallant M., Gareau Y., Giffen P.R., Labelle M., Lazebnik Y.A.,
RA Munday N.A., Raju S.M., Smolins M.E., Yamin T.-T., Li V.L.,
RA Miller D.K.,
RT "Identification and inhibition of the ICE/CED-3 protease necessary
RT for mammalian apoptosis.";
RL Nature 376:37-43(1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 28-277.
RX MEDLINE=96266352; PubMed=8673606;
RA Labella M., Peterson B.P., Rasper D.M., Ruel R., Vailancourt J.P.,
RA Thornberry N.A., Becker J.W.,
RT "The three-dimensional structure of apopain/CP32, a key mediator of
RT apoptosis.";
RL Nat. Struct. Biol. 3:619-625(1996).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277.
RX MEDLINE=97197830; PubMed=9045680;
RA Mitl P.R.E., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,
RA Priestle J.P., Tomaseili K.J., Grueter M.G.,
RT "Structure of recombinant human CPP32 in complex with the
RT tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl ketone.";
RL J. Biol. Chem. 272:6539-6547(1997).
RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=20283632; PubMed=10821855;
RA Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
RA Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
RA Levy M.A., Demolfi W.E., Jr., Keller P.M., Tomaszek T., Head M.S.,
RA Ryan M.D., Halliwaenger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
RA Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
RA Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.,
RT "Potent and selective nonpeptide inhibitors of caspases 3 and 7
RT inhibit apoptosis and maintain cell functionality.";
RL J. Biol. Chem. 275:16007-16014(2000).
RN [10]
RP PROCESSING.
RX MEDLINE=96353838; PubMed=8755496;
RA Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srinivasula S.M.,
RA Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomaseili K.J.,
RA Litwack G., Alnemri E.S.,
RT "In vitro activation of CPP32 and Mch3, a novel human
RT apoptotic cysteine protease containing two FAD-like domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
RN [11]
RP CLEAVAGE OF HUNTINGTIN.
RX MEDLINE=96331285; PubMed=8696339;
RA Goldberg Y.P., Nicholson D.W., Rasper D.M., Kalchman M.A., Koide H.B.,
RA Graham R.K., Bromm M., Kazemi-Esfarjani P., Thornberry N.A.,
RA Vailancourt J.P., Hayden M.R.,
RT "Cleavage of huntingtin by apopain, a proapoptotic cysteine protease,
RT is modulated by the polyglutamine tract.";
RL Nat. Genet. 13:442-449(1996).
RN [12]
RP FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9. Involved in the
CC cleavage of huntingtin.
CC - ENZYME REGULATION: Inhibited by isatin sulfonamides.
CC - SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit.
CC - SUBCELLULAR LOCATION: Cytoplasmic.
CC - TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
CC and kidney. Moderate levels in brain and skeletal muscle, and low
CC in testis. Also found in many cell lines, highest expression in
CC cells of the immune system.
CC - PTM: CLEAVAGE BY GRANZYME B, ADAM-1, CASPASE-6, -8 AND -10
CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC AND VICE VERSA.
CC - SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC -----
DR EMBL, U13737; AAA65015.1; -;
DR EMBL, U13738; AAB60355.1; -;
DR EMBL, U26943; AAN74929.1; -;
DR EMBL, AJ413269; CAC88866.1; -;
DR EMBL, AY1219866; AAO25654.1; -;
DR EMBL, BC016926; AAH16926.1; -;
DR PIR, A55315; A55315-;
DR PDB, 1PAU; 07-JUN-97.
DR PDB, 1CP3; 24-DEC-97.
DR PDB, 1CFW; 23-JUN-00.
DR MEROPS, C14.003; -;
DR Genew; HGNC:1504; CASP3.
DR MIM; 60636; -;


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DR GO; GO:0004208; F.caspase-3 activity; TAS.
DR GO; GO:0008624; P.induction of apoptosis by extracellular sig. . .; TAS.
DR GO; GO:0008629; P.induction of apoptosis by intracellular sig. . .; TAS.
DR GO; GO:0009405; P.pathogenesis; TAS.
DR InterPro; IPR002138; ICB p10.
DR InterPro; IPR001309; ICB p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Hydrolyase; Thiol protease; Zymogen; Apoptosis; Polymorphism;
KM 3D-structure.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT SITE 121 121
FT ACT SITE 163 163
FT ACT SITE 190 190
FT VARIANT 190 190
FT CONFLICT 31 36
FT STRAND 36 36
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 66
FT HELIX 67 80
FT TURN 81 82

Query Match 23.9%; Score 179.5; DB 1; Length 277;
Best Local Similarity 30.7%; Pred. No. 2.9e-09;
Matches 46; Conservative 25; Mismatches 60; Indels 19; Gaps 5;

9 EEKYDWSGAALALILCVTK-----AREGSEEDLALHEMFROLRSESTMKRDPYA 58
34 DMSYKMDYPMGACIIINNNKFNHSTGMTSRSGTDVDAANLRETFENLKYEVHNNKNDLTR 93
59 EQGQEELEKFOQALDSREDPVSACFVYLMAHGREGLKSGDG--EMVKLENLFEALNNKN 116
94 EEVEIMRDVSKEDSHRSSFVC---VLSHGEGGIIFGNGPYDLKKTINFF---RGDR 147
117 COALPAKPYVYIIQACRGEGRPDQ-ETVVG 145
148 CRSLTGKPKLFIIOACRGTELDGSIETDSG 177

Db
QY 117 COALPAKPYVYIIQACRGEGRPDQ-ETVVG 145
DB 148 CRSLTGKPKLFIIOACRGTELDGSIETDSG 177

RESULT 12
ICBA_XENLA STANDARD; PRT; 386 AA.
AC P55865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-1 beta convertase precursor A precursor (EC 3.4.22.-)
DE (XCF-A) (Caspase-1A) (CASP-1A).
GN CASP1A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN [1] SEQUENCE FROM N.A.
RA Yaocita Y., Nakajima K.;
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----

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CC or send an email to license@isb-sb.ch).
CC -----
DR EMBL; D89783; BA014017.1; -.
DR HSP; P29466; IICB.
DR MEROPS; C14.DPM; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICB p10.
DR InterPro; IPR001309; ICB p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR Hydrolyase; Thiol protease; Zymogen.
KM 3D-structure.
FT PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT SITE 121 121
FT ACT SITE 163 163
FT ACT SITE 190 190
FT VARIANT 190 190
FT CONFLICT 31 36
FT STRAND 36 36
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 66
FT HELIX 67 80
FT TURN 81 82

Query Match 23.7%; Score 178; DB 1; Length 386;
Best Local Similarity 29.5%; Pred. No. 5.8e-09;
Matches 49; Conservative 26; Mismatches 57; Indels 34; Gaps 5;

4 PRLEERK-----YDM-----SGAALALILCVTK-----AREGSEEDLALHEMF 44
116 PCSAEFFPKIQDTGCKIYDVRKRGKGLALICNEKFNLENRGAQKVDLQMTYLN 175
45 QLRFEESTMKRDPYAEFOELEKFOQALDSREDPVSACFVYLMAHGREGLKSGDG-- 101
176 ELGQVQHNNLNLTKEVMKVKKEF--AAQEHADSDSTFIWLSHGQGVCGDPSKTE 233
102 -----MKLENLFEALNNKNCOALPAKPYVYIIQACRGEP 137
234 KEGQYEVNMLEIDEIFSTFNVNCCKLNKPKVYIIQACRGENK 279

Db
QY 102 -----MKLENLFEALNNKNCOALPAKPYVYIIQACRGEP 137
DB 234 KEGQYEVNMLEIDEIFSTFNVNCCKLNKPKVYIIQACRGENK 279

RESULT 13
IIBC_RAT STANDARD; PRT; 402 AA.
AC P43527;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-1 beta convertase precursor (IL-1BC) (EC 3.4.22.36) (IL-1
DE beta converting enzyme) (ICE) (Interleukin-1 beta converting enzyme)
DE (P45) (Caspase-1) (CASP-1).
GN CASP1 OR IIBC OR IL1BC.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN [1] SEQUENCE FROM N.A.
RA Tissue=Skin;
RC MEDLINE=95299018; PubMed=7780029;
RA Keane K.W., Giegel D.A., Lipinski W.J., Callahan M.J.,
RA Shivers B.D.;
RT "Cloning, tissue expression and regulation of rat interleukin 1 beta
RT converting enzyme.";

```

Qy	19	LAAILCYE-----KAREGSEEDIDALEHMRPQIRFESTAKRDPDPAQFOEELKFOQAD	73
Db	163	LAAILCNTDPQHSRRVAGAVDLREKLLTLQDLYGVKAKENITALEMKELKEFAPACE	222
Qy	74	SREDPVSCAFVYLMAG-BEGF-----LKGEDEGMVLELFEALNNKNCQALRAXPRVYI	128
Db	223	HKTS--DSTFLVFMSHLOEGIGITYSNEVADILKVDTLFGQMMNTLKPSLKDREKVI	280
Qy	129	IQACRGEOR	137
Db	281	IQACRGEQ	289
RESULT 14			
ICB	XENLA	STANDARD;	PRT; 382 AA.
ID	ICB_XENLA		
AC	P55867;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DE	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Interleukin-1 beta convertase homolog B precursor (EC 3.4.22.-)		
DE	(XIC-B) (Caspase-1B) (CASP-1B).		
GN	CASP1B.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;		
OC	Amphibia, Batrachia, Anura, Mesobatrachia, Pipidae, Pipidae;		
OX	Xenopodinae; Xenopus.		
NP	NCBI_Taxid=83355;		
RP	SEQUENCE FROM N.A.		
RA	Nakajima K.;		
RL	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).		
CC	-1- SIMILARITY: Belongs to peptidase family C14.		
CC	-1- SIMILARITY: Contains 1 CARD domain.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL: D89785; BA114019.1; -.		
DR	HSSP: P29466; IICE.		
DR	MEROPS; C14.OPW; -.		
DR	InterPro: IPR001315; CARD.		
DR	InterPro: IPR002138; ICE_P10.		
DR	InterPro: IPR001309; ICE_P20.		
DR	InterPro: IPR002398; Peptidase_C14.		
DR	Pfam: PF00619; CARD; 1.		
DR	Pfam: PF00656; Peptidase_C14; 1.		
DR	PRINTS; PR00376; TLHCENZYME.		
DR	SMART; SM00114; CARD; 1.		
DR	SMART; SM00115; CASC; 1.		
DR	PROSITE; PS50209; CARD; 1.		
DR	PROSITE; PS50123; CASPASE_CYS_1.		
DR	PROSITE; PS01121; CASPASE_HIS_1.		
DR	PROSITE; PS50207; CASPASE_P10; 1.		
DR	PROSITE; PS50208; CASPASE_P20; 1.		
DR	Hydrolase; Thiol protease; Zymogen.		
FT	PROPEP	1	
FT	CHAIN	?	POTENTIAL.
FT	DOMAIN	22	INTERLEUKIN-1 BETA CONVERTASE HOMOLOG B.
FT	ACT_SITE	216	BY SIMILARITY.
FT	ACT_SITE	270	BY SIMILARITY.
Q	SEQUENCE	382 AA; 43389 MW; 81DFFB7BF3C2230F CRC64;	

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QY 4 PRSLIEEK-YDMG-----AALALILC-----VTKAREGSEEDLDALHEHMR 44
DB 114 PCSAEFEFNIIYDSHDKIYEVNERGRKRRLALILNETFQSMSERRGAKLLEGNKILN 173
QY 45 QLRPESTKRPDPTAFOFQELKEKFOQALDSREDFV--SCAFVYLAHAREGFLKEDGE- 101
DB 174 ELGYVQVQHTNLTKAEWKAKKEFA---AREEHADSDSTFVLSHGDKEVCITDKK 229
QY 102 -----WKLENTFEALNNKCOALRAKPKYIIIOACRGQRDQETVGGD 146
DB 230 TENGYGVTNLLOVEIFSTFNNVNCSTRMDKPKXIIIOACGNGOG--GELYRDD 283

RESULT 15
11BC_FELCA STANDARD; PRT; 410 AA.
ID 11BC_FELCA STANDARD; PRT; 410 AA.
AC 09MZV6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-1 beta convertase precursor (IL-1BC) (BC 3.4.22.36) (IL-1
  beta converting enzyme) (ICE) (Interleukin-1 beta converting enzyme)
DE (P45) (Caspase-1) (CASP-1).
GN CASP1 OR IL1BC.
OS Felis silvestris catus (cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9695;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284946; PubMed=10826695;
RA Taylor S., Hanlon L., McGillivray C., Gault E.A., Argyle D.J.,
RT Onions D.E., Nicolson L.;
RT "Cloning and sequencing of feline and canine ice-related cDNAs
  encoding hybrid caspase-1/caspase-13-like propeptides.";
RL DNA Seq. 10:387-394 (2000).
CC -1- FUNCTION: Thiol protease that cleaves IL-1 beta between an Asp and
  an Ala, releasing the mature cytokine which is involved in a
  variety of inflammatory processes (By similarity).
CC -1- CATALYTIC ACTIVITY: Release of interleukin 1-beta by specific
  cleavage at 116-Asp-1-Ala-117 and 27-Asp-1-Gly-28 bonds in
  precursor. Also hydrolyzes the small-molecule substrate, Ac-Tyr-
  Val-Ala-Asp-1-NHMe.
CC -1- SUBUNIT: Tetramer that consists of two heterodimers of a 20 kDa
  (p20) and a 10 kDa (p10) subunits. The p20 subunit can also form a
  heterodimer with the epsilon isoform which then has an inhibitory
  effect (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: The two subunits are derived from the precursor sequence by
  autocatalytic mechanism.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF135968; AAF64389.1; -.
DR HSSP; P29466; 1ICE.
DR MEROPS; C14.024; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASG; 1.

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DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Zymogen; Polymorphism.
FT PROPEP 1 119
FT CHAIN 120 296
FT PROPEP 297 322
FT CHAIN 323 410
FT DOMAIN 1 91
FT ACT_SITE 235 235
FT ACT_SITE 284 284
FT VARIANT 136 136 H -> R.
SQ SEQUENCE 410 AA; 46051 MW; 2B8B99C0074A0C5 CRC64;

Query Match 23.3%; Score 175.5; DB 1; Length 410;
Best Local Similarity 31.3%; Pred. No. 1,1e-08;
Matches 41; Conservative 26; Mismatches 45; Indels 19; Gaps 4;

QY 19 IALILCVT-----KAREGSEEDLDALHEHMRQLRESTMKRPDPTAFOFQELKEKFOQALD 73
DB 162 IALILCVTTFDHLSPKRGADLDVAQMRRLTLDTGISVHIKEELTKADMESELRAFAAPE 221
QY 74 SREDPVSCAFVYLAHAREGFLKG-----EDGEVWKLNTFEALNNKCOALRAKP 124
DB 222 HKSS--DSFLVFMH--GILSGICGTKYSAGDPDVLAYDTIFQIFNNRCLSLDKRP 276
QY 125 KYIIIOACRGE 135
DB 277 KYIIIOACRGE 287

```

Search completed: July 12, 2004, 13:48:22
Job time : 7.2367 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Inc.

OM protein - protein search, using sw model

Run on: July 12, 2004, 13:43:31 ; Search time 29.8636 Seconds
(without alignments)
1542.533 Million cell updates/sec

Title: US-10-068-564-5_COPY_1_146
Perfect score: 752
Sequence: 1 MSNPRSLREKXKXMSGAALA.....YIQACRGEQRPGETGVGD 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPTRMBL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	210	27.9	435	4	Q9BUP7
2	210	27.9	452	11	Q8C9H7
3	207	27.5	452	11	Q8K241
4	205	27.3	452	11	Q55194
5	204.5	27.2	399	13	Q9IB63
6	198	26.3	423	13	Q9IB67
7	197	26.2	312	4	Q86UJ3
8	196	26.1	415	13	Q80UM6
9	196	26.1	419	13	Q7ZXD2
10	195	25.9	403	13	Q90WU0
11	194	25.8	393	11	Q9R0S9
12	194	25.8	453	11	Q8C300
13	194	25.8	454	11	Q9R0T0
14	194	25.8	454	11	Q8C309
15	192	25.5	343	11	Q9WU16
16	191.5	25.5	482	13	Q90WU1

17	191	25.4	402	11	Q8K419	Q8K419 meriones un
18	181.5	24.1	383	13	Q919L7	Q919L7 brachydanio
19	178	23.7	454	11	Q9JHK1	Q9JHK1 rattus norv
20	177	23.5	402	11	Q9JW32	Q9JW32 rattus norv
21	175.5	23.3	182	6	Q77623	Q77623 ovis aries
22	174.5	23.2	500	13	Q9IB64	Q9IB64 xenopus lae
23	173.5	23.1	290	13	Q81B58	Q81B58 oryzias lat
24	173	23.0	303	11	Q88550	Q88550 rattus norv
25	171.5	22.8	277	6	Q8MTU1	Q8MTU1 felis silve
26	171	22.7	316	5	Q817B0	Q817B0 geodia cydo
27	171	22.7	426	5	Q816Y2	Q816Y2 geodia cydo
28	170	22.6	420	11	Q920D5	Q920D5 rattus norv
29	169	22.5	419	11	Q8BSX6	Q8BSX6 mus musculu
30	167	22.2	482	11	Q9JHX4	Q9JHX4 rattus norv
31	167	22.2	520	13	Q9IB62	Q9IB62 xenopus lae
32	165	21.9	373	11	Q91XW7	Q91XW7 rattus norv
33	164.5	21.9	283	13	Q42284	Q42284 gallus gall
34	164.5	21.9	417	5	Q9YIU6	Q9YIU6 pristionchu
35	163.5	21.7	277	6	Q95NDS	Q95NDS sus scrofa
36	163.5	21.7	277	6	Q8MTC3	Q8MTC3 oryctolagus
37	162.5	21.6	277	6	Q8MKI5	Q8MKI5 canis fami
38	162.5	21.6	313	11	Q8CHV5	Q8CHV5 mus musculu
39	161.5	21.5	289	5	Q86FL0	Q86FL0 anopheles s
40	157	20.9	299	5	Q81955	Q81955 spodoptera
41	156	20.7	318	13	Q9IB65	Q9IB65 xenopus lae
42	156	20.7	383	11	Q99M88	Q99M88 rattus norv
43	155	20.6	283	13	Q93417	Q93417 gallus gall
44	154.5	20.5	476	13	Q918U5	Q918U5 brachydanio
45	154	20.5	293	5	Q819V7	Q819V7 bombyx mori

ALIGNMENTS

RESULT ID	1	PRELIMINARY:	PRT:	435 AA.
Q9BUP7	Q9BUP7	Q9BUP7		
AC	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Similar to caspase 2 (Neutral cell expressed, developmentally down-regulated 2).			
OS	Homo sapiens (human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kalnine N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S.,			
RA	Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,			
RA	Pfeil M., Farmer A.,			
RT	"Cloning of human full-length cDNAs in BD Creator(TM) System Donor vector."			
RT	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC002427; AA02427.1; -			
DR	EMBL; BT007240; AAP5904.1; -			
DR	HSSP; P29466; ITCE.			
DR	GO; GO:0005622; C:intracellular; IEA.			
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.			
DR	GO; GO:0006933; F:caspase activity; IEA.			
DR	GO; GO:0008233; F:peptidase activity; IEA.			
DR	GO; GO:0006915; P:apoptosis; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR001315; CARD.			
DR	InterPro; IPR002138; ICE_P10.			
DR	InterPro; IPR001309; ICE_P20.			
DR	InterPro; IPR002398; Peptidase_C14.			

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DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS50209; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROTEASE.
SQ SEQUENCE 435 AA; 48869 MW; 10CF5A51F9369E57 CRC64;

Query Match 27.9%; Score 210; DB 4; Length 435;
Best Local Similarity 37.5%; Pred. No. 2.2e-11;
Matches 42; Conservative 29; Mismatches 39; Indels 2; Gaps 2;

QY 29 REGSEEDDALAHMFRQLRFESTMKRDPPTAQFOEELKFOQALDSREDPVSCAFVYIMA 88
DB 202 RSGGDVDTHTTVTLFRLIGYVNVHLHDQTAQEMQEKLNQFAQ-LPAHRYTDSCTV-VALLS 259
QY 89 HGRBGFLLKGEDEWVLENTLFEALNNKNCQALRAKPKYITIOACRGEQDPG 140
DB 260 HGVEGATYGVGDKLLQLOEVFRLFDNANCPSLQNKPKMFITQACRGEQDPG 311

RESULT 2
Q8C9H7 PRELIMINARY; PRT; 452 AA.
AC O8C9H7;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
GN Caspase 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=2354663; PubMed=12466851;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK042072; BAC31153.1; -.
DR MGD; MGI:97295; Casp2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50689 MW; C3715908508619CA CRC64;

Query Match 27.9%; Score 210; DB 11; Length 452;
Best Local Similarity 38.4%; Pred. No. 2.3e-11;
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Matches 43; Conservative 26; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDDALAHMFRQLRFESTMKRDPPTAQFOEELKFOQALDSREDPVSCAFVYIMA 88
DB 219 RSGGDVDTHTTVTLFRLIGYVNVHLHDQTAQEMQEKLNQFAQ-LPAHRYTDSCTV-VALLS 276
QY 89 HGRBGFLLKGEDEWVLENTLFEALNNKNCQALRAKPKYITIOACRGEQDPG 140
DB 277 HGVEGATYGVGDKLLQLOEVFRLFDNANCPSLQNKPKMFITQACRGEQDPG 328

RESULT 3
Q8K241 PRELIMINARY; PRT; 452 AA.
AC Q8K241;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
GN Caspase 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034262; AAH34262.1; -.
DR MGD; MGI:97295; Casp2.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BCENZYM.
DR SMART; SM00114; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50661 MW; A4DE25A712FAB855 CRC64;

Query Match 27.5%; Score 207; DB 11; Length 452;
Best Local Similarity 37.5%; Pred. No. 4.4e-11;
Matches 42; Conservative 27; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDDALAHMFRQLRFESTMKRDPPTAQFOEELKFOQALDSREDPVSCAFVYIMA 88
DB 219 RSGGDVDTHTTVTLFRLIGYVNVHLHDQTAQEMQEKLNQFAQ-LPAHRYTDSCTV-VALLS 276
QY 89 HGRBGFLLKGEDEWVLENTLFEALNNKNCQALRAKPKYITIOACRGEQDPG 140
DB 277 HGVEGATYGVGDKLLQLOEVFRLFDNANCPSLQNKPKMFITQACRGEQDPG 328

RESULT 4
O55194 PRELIMINARY; PRT; 452 AA.
AC O55194;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
OS Rattus norvegicus (Rat).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98087427; PubMed=9427555;
RA Sato N., Milligan C.E., Uchiyama Y., Oppenheim R.W.;
RT "Cloning and expression of the cDNA encoding rat caspase-2."
RL Gene 202:127-132(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA Jin K.U., Simon R.P., Graham S.H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U77933; AAB96379.1; -.
DR EMBL; AF136231; AAD33684.1; -.
DR PIR; J06507; J06507.
DR HSSP; P29466; 1ICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR002398; Peptidase_C14.
DR InterPro; IPR001309; ICE_p20.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 452 AA; 50728 MW; 03F9D096BB741CE3 CRC64;

Query Match 27.3%; Score 205; DB 11; Length 452;
Best Local Similarity 37.5%; Pred. No. 6,7e-11;
Matches 42; Conservative 21; Mismatches 41; Indels 2; Gaps 2;

QY 29 REGSEEDLDALHEMFRLQRFESTMKRDPDTAEQFOEELKEKQALDSREDPVSCAFVVLMA 88
Db 219 RSGGDVHTLTVLTLFKLGVNVHLYDQTQEMQEKLNPAQ-LPAHRTVDSCLVALLS 276
QY 89 HGERGFLKEDGEMVLENIPEALNNKQCALRAKPKVYITQACRGQRDPG 140
Db 277 HGEVGGIYVDKILQLQEVFRLLFDNANCPSLQNKPMFPIQACRGDETDRG 328

RESULT 5
Q91B63 PRELIMINARY; PRT; 399 AA.
ID Q91B63
AC Q91B63
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase-9.
GN XCASPASE-9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
family."
RL J. Biol. Chem. 275:10484-10491(2000).

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DR EMBL; AB038172; BAA94750.1; -.
DR HSSP; Q15806; 1ODU.
DR MEROPS; C14.010; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
SQ SEQUENCE 399 AA; 44772 MW; EE2A269719064F9F CRC64;

Query Match 27.2%; Score 204.5; DB 13; Length 399;
Best Local Similarity 31.2%; Pred. No. 6,5e-11;
Matches 49; Conservative 26; Mismatches 61; Indels 21; Gaps 4;

QY 2 SNPRSLFEERK-YDMGALALILICVT-----KAREGSEEDLDALHEMFRLQRFES 50
Db 125 SRKGLIDKKKDYPMSSDDPIGFCLITNNMNFHETGLSTGTSDIDRDLANRRKSHFEV 184
QY 51 TMKRDPDTAEQFOEELKEKQALDSREDPVSCAFVVLMAHGRE-----GFLKGEDGEMV 103
Db 185 TVKDNITGQAMDHQLALDDQHSLOD-----CCIVLTLSHGCERHRIQFGVGYGTGIRI 241
QY 104 KLENLFEALNNKQCALRAKPKVYITQACRGQRDPG 140
Db 242 PVERIVSYFNNGSKPSLRGPKIFITQACGQDXKRG 278

RESULT 6
Q91B67 PRELIMINARY; PRT; 423 AA.
ID Q91B67
AC Q91B67
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase-2.
GN XCASPASE-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209426; PubMed=10744739;
RA Nakajima K., Takahashi A., Yacita Y.;
RT "Structure, expression and function of the Xenopus laevis caspase
family."
RL J. Biol. Chem. 275:10484-10491(2000).
DR EMBL; AB038168; BAA94746.1; -.
DR HSSP; P29466; 1ICE.
DR MEROPS; C14.006; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

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DR InterPro: IPR001315; CARD.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00619; CARD; 1.
DR PRINTS: PR00376; IL1BCENZYM.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 423 AA; 47123 MW; E91EB1FD13F01FD CRC64;
Query March 26.3%; Score 198; DB 13; Length 423;
Best Local Similarity 35.9%; Pred. No. 2.8e-10;
Matches 42; Conservative 26; Mismatches 37; Indels 12; Gaps 2;
QY 29 REGSEEDLDALHMFRLQRFESTMKRDPPTAEQFOELEKFGQAIDSRDPVSCAF 83
Db 187 RCGGEVDLASLEKLFSSILGYQVDVRCNLNAGSMSSQLGAFSALPVHSLDS-----CV 239
QY 84 VVLMHGRGFLKEDGEMVXLENTFEALNNKNCQALRAKPKVYIIQACRGSGDPG 140
Db 240 VVLSHGLDGAIVGTGKLVQLQEVFTALDNHCPQLQNKPKMFFIQACRGSEETDRG 296
RESULT 7
Q86UJ3 PRELIMINARY; PRT; 312 AA.
AC Q86UJ3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein CASP2.
GN CASP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Doeber A., Martinka S., Maupin R.;
RT "The sequence of Homo sapiens BAC clone RP11-55613.";
RN Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Waterston R.H.;
RN Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RN Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Waterston R.;
RN [5]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RN Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC073342; AAP2347.1; -;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caseinase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001309; ICE_p20.

DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; IL1BCENZYM.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hypothetical protein.
SQ SEQUENCE 312 AA; 34866 MW; E518F4B69A7D1414 CRC64;
Query March 26.2%; Score 197; DB 4; Length 312;
Best Local Similarity 37.7%; Pred. No. 2.5e-10;
Matches 40; Conservative 27; Mismatches 37; Indels 2; Gaps 2;
QY 29 REGSEEDLDALHMFRLQRFESTMKRDPPTAEQFOELEKFGQAIDSRDPVSCAFVILMA 88
Db 188 RSGGDVHSTLVTLFKILGVDVHLCQITAGEMOEKLNQFAQ-LPAHRVTDSC-IVALIS 245
QY 89 HGRBGLKEDGEMVXLENTFEALNNKNCQALRAKPKVYIIQACRG 134
Db 246 HGVEGALYGVGDKLQLQEVFQLFDNANCPSLQNKPKMFFIQACRG 291
RESULT 8
Q801M6 PRELIMINARY; PRT; 415 AA.
AC Q801M6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RN Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049286; AAH49286.1; -;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caseinase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; IL1BCENZYM.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hypothetical protein.
SQ SEQUENCE 415 AA; 46542 MW; CD953432340BE8B CRC64;
Query March 26.1%; Score 196; DB 13; Length 415;
Best Local Similarity 36.6%; Pred. No. 4.2e-10;
Matches 41; Conservative 26; Mismatches 43; Indels 2; Gaps 2;
QY 29 REGSEEDLDALHMFRLQRFESTMKRDPPTAEQFOELEKFGQAIDSRDPVSCAFVILMA 88
Db 183 RCGGEVDLASLEKLFSSILGYQVDVRCNLNAGSMSSQLGAFSALPVHSLDSGC-IVALIS 240

DR Pfam: PF00619; CARD; 1.
DR PRINTS; PR00376; ILIBENZYM. 1.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 393 AA; 42975 MW; CA889475E5DD632 CRC64;

Query Match 25.8%; Score 194; DB 11; Length 393;
Best Local Similarity 37.4%; Pred. No. 6.1e-10;
Matches 46; Conservative 17; Mismatches 42; Indels 18; Gaps 3;

QY 29 REGSEEDLDALAHMFRQLEFESTMKRDPPTAQ-----FOELEKFGQALDSREDPVSCAFV 84
Db 218 RTGSNLDKDLKLEHFRFWLRFVVEVKNLDTAKKMTALMEMAHRNRALD-----CFVV 270

QY 85 VLMAHGRE-----GFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYITIQACRGEOR 137
Db 271 VILSHGQASHLQPPGAVYGTGCGSVSIEKIVNIFNSGCGPSLGKPKLFTFIQACGGEOR 330

QY 138 DPG 140
Db 331 DHG 333

RESULT 12
Q8C300 ID Q8C300 PRELIMINARY; PRT; 453 AA.
AC Q8C300;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 9 (Fragment).
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team.
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK085152; BAC39378.1; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR002139; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
FT NON TER 1
SQ SEQUENCE 453 AA; 49847 MW; 8F7D1C50F7ABA68F CRC64;

Query Match 25.8%; Score 194; DB 11; Length 454;
Best Local Similarity 37.4%; Pred. No. 7.2e-10;
Matches 46; Conservative 17; Mismatches 42; Indels 18; Gaps 3;

QY 29 REGSEEDLDALAHMFRQLEFESTMKRDPPTAQ-----FOELEKFGQALDSREDPVSCAFV 84
Db 217 RTGSNLDKDLKLEHFRFWLRFVVEVKNLDTAKKMTALMEMAHRNRALD-----CFVV 269

QY 85 VLMAHGRE-----GFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYITIQACRGEOR 137
Db 270 VILSHGQASHLQPPGAVYGTGCGSVSIEKIVNIFNSGCGPSLGKPKLFTFIQACGGEOR 329

QY 138 DPG 140
Db 330 DHG 332

RESULT 13
Q9ROT0 ID Q9ROT0 PRELIMINARY; PRT; 454 AA.
AC Q9ROT0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase9.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20001956; PubMed=10529400;
RA Fujita E., Jinbo A., Matuzaki H., Konishi H., Kikkawa U., Momoi T.;
RT "Akt phosphorylation site found in human caspase-9 is absent in mouse
RT caspase-9."
RL Biochem. Biophys. Res. Commun. 264:550-555(1999).
DR EMBL; AB019600; BAA86895.1; -.
DR PIR; JCT123; JCT123.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.010; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR002139; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CARD; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 454 AA; 50051 MW; 4614989A7E23850F CRC64;

Query Match 25.8%; Score 194; DB 11; Length 454;
Best Local Similarity 37.4%; Pred. No. 7.2e-10;
Matches 46; Conservative 17; Mismatches 42; Indels 18; Gaps 3;

QY 29 REGSEEDLDALAHMFRQLEFESTMKRDPPTAQ-----FOELEKFGQALDSREDPVSCAFV 84
Db 218 RTGSNLDKDLKLEHFRFWLRFVVEVKNLDTAKKMTALMEMAHRNRALD-----CFVV 270

QY 85 VLMAHGRE-----GFLKGEDEGMVKLENLFEALNNKNCQALRAKPKVYITIQACRGEOR 137

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Db 271 VILSHGCCASHLQEPGAVYGTGCSVSTIEKIVNIFNNGSGCPSLGKPKLFTIQACGGEOK 330
QY 138 DPG 140
Db 331 DHG 333

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RESULT 14

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08C309 PRELIMINARY; PRT; 454 AA.
ID 08C309
AC 08C309;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase 9.
GN CASP9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.
RL Nature 420:563-573(2002).
DR EMBL; AK085095; BAC39365.1; -.
DR MGD; MGI:1277950; Casp9.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR PRINTS; PR00376; ILICENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SQUENCE 454 AA; 49979 MW; 438A67EA6A6EE78 CRC64;

```

Query Match 25.8%; Score 194; DB 11; Length 454;

Best Local Similarity 37.4%; Pred. No. 7.2e-10; Matches 46; Conservative 17; Mismatches 42; Indels 18; Gaps 3;

```

QY 29 RRGSEEDLDALHEMFROLPFESTMKRDPPTAEQ---FQSELEKFOQAIDSRDPVSCAFV 84
Db 218 RTGSNDLRDKLHEHFRWIRFVRYKNDITAKKMTALMEMHRHNRALD-----CFVV 270
QY 85 VLMAGRE-----GFLKGEDGEMVYKLENLFEALNNKNCQALRAKPKVYITIQACRGEOR 137
Db 271 VILSHGCCASHLQEPGAVYGTGCSVSTIEKIVNIFNNGSGCPSLGKPKLFTIQACGGEOK 330
QY 138 DPG 140
Db 331 DHG 333

```

RESULT 15

ID Q9WU16 PRELIMINARY; PRT; 343 AA.

```

AC Q9WU16;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase-25.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Jin K.U.; Graham S.H.; Simon R.P.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF136232; AAD33685.1; -.
DR HSP; P29466; IICE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILICENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SQUENCE 343 AA; 38003 MW; 0292D6130C63F641 CRC64;

```

Query Match 25.5%; Score 192; DB 11; Length 343;

Best Local Similarity 37.7%; Pred. No. 8.1e-10; Matches 40; Conservative 25; Mismatches 39; Indels 2; Gaps 2;

```

QY 29 RRGSEEDLDALHEMFROLPFESTMKRDPPTAEQFQSELEKFOQAIDSRDPVSCAFVYMA 88
Db 219 RSGGDVDDHTLVTLVTLFYLGNVHVLYDQTAQEWQEKLNFAQ--LPAHRTVDSG--IVALLS 276
QY 89 HGESEGLKGEDGEMVYKLENLFEALNNKNCQALRAKPKVYITIQACRG 134
Db 277 HGEVGGIYGVGKLDQLQEVFRFLPDANCPSLQNKRFMTFIQACRG 322

```

Search completed: July 12, 2004, 13:50:14

Job time : 29.8636 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:39:36 ; Search time 28.562 Seconds
(without alignments)
949.674 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242
Perfect score: 487
Sequence: 1 EIVWIKDSFGTIPPTDNL.....KARKTNPETGSTRKRLYLQ 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_28Jan04:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	487	100.0	214	3	AA93216 Amino aci
2	487	100.0	229	3	AA68865 Amino aci
3	487	100.0	242	3	AA93214 Amino aci
4	487	100.0	242	5	AA677980 Full-leng
5	487	100.0	242	5	AA677984 Full-leng
6	357	73.3	257	3	AA68864 Amino aci
7	357	73.3	281	2	AA93552 Mouse cas
8	357	73.3	281	3	AA93213 Amino aci
9	195	40.0	234	5	AAU72882 Human asp
10	195	40.0	398	5	ABG76499 DNA encod
11	143	29.4	230	3	AA93215 Amino aci
12	129.5	26.2	503	2	AA45295 Ced-3 mut
13	129.5	26.2	494	4	AB663301 Drosophila
14	127.5	26.2	503	2	AA45286 Ced-3 mut
15	127.5	26.2	503	2	AA45304 Ced-3 mut
16	127.5	26.2	503	2	AA45309 Ced-3 mut
17	127.5	26.2	503	2	AA45311 Ced-3 mut
18	127.5	26.2	503	2	AA45292 Ced-3 mut
19	127.5	26.2	503	2	AA45294 Ced-3 mut
20	127.5	26.2	503	2	AA45297 Ced-3 mut
21	127.5	26.2	503	2	AA45317 Ced-3 mut
22	127.5	26.2	503	2	AA45317 Ced-3 mut
23	127.5	26.2	503	2	AA45288 Ced-3 mut
24	127.5	26.2	503	2	AA45290 Ced-3 mut
25	127.5	26.2	503	2	AA45299 Ced-3 mut

26	127.5	26.2	503	2	AA45308 Ced-3 mut
27	127.5	26.2	503	2	AA45314 Ced-3 mut
28	127.5	26.2	503	2	AA45316 Ced-3 mut
29	127.5	26.2	503	2	AA45324 Ced-3 mut
30	127.5	26.2	503	2	AA45278 Ced-3 mut
31	127.5	26.2	503	2	AA45276 Ced-3 mut
32	127.5	26.2	503	2	AA45289 Ced-3 mut
33	127.5	26.2	503	2	AA45291 Ced-3 mut
34	127.5	26.2	503	2	AA45300 Ced-3 mut
35	127.5	26.2	503	2	AA45310 Ced-3 mut
36	127.5	26.2	503	2	AA45293 Ced-3 mut
37	127.5	26.2	503	2	AA45280 Ced-3 mut
38	127.5	26.2	503	2	AA45302 Ced-3 mut
39	127.5	26.2	503	2	AA45303 Ced-3 mut
40	127.5	26.2	503	2	AA45313 Ced-3 mut
41	127.5	26.2	503	2	AA45318 Ced-3 mut
42	127.5	26.2	503	2	AA45281 Ced-3 mut
43	127.5	26.2	503	2	AA45282 Ced-3 mut
44	127.5	26.2	503	2	AA45283 Ced-3 mut
45	127.5	26.2	503	2	AA45287 Ced-3 mut

ALIGNMENTS

RESULT 1
AA93216
ID AA93216 standard; protein; 214 AA.
XX
AC AA93216;
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of a human caspase-14 splice variant.
XX
KW Caspase-14; cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Active-site 102..106
XX
XX WO200028047-A1.
XX
PD 18-MAY-2000.
XX
PF 29-OCT-1999; 99WO-US025523.
XX
PR 06-NOV-1998; 98US-00187789.
XX
PA (UYBE-) UNTIV JEFFERSON THOMAS.
XX
PI Alnemri ES, Fernandez-Alnemri T;
XX WPI, 2000-376558/32.
XX N-PSDB; AA415166.
XX
PT Novel nucleic acids encoding cell death specific protease termed caspase-
PT 14 useful for treating cancers by stimulating apoptosis.
XX
PS Claim 42; Fig 9; 78pp; English.
XX
XX The present sequence represents a human caspase-14 splice variant. The
XX polypeptide is a cell death specific protease, and is an apoptosis
XX stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
XX -14 antibodies are useful for treating or reducing the severity of
XX pathological conditions associated with increased or decreased levels of
XX apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
XX diseases and ischemic injury are treated by administering anti-caspase-14
XX antibodies. The antibody is useful for determining the presence of the
XX level of caspase-14 in tissue sample and also for the isolation of
XX caspase-14 with apoptotic activity or in screening assay to identify an

CC agent that inhibits heterodimer or heterotetramer formation and
CC therefore, apoptosis
XX
SQ Sequence 214 AA;

Query Match 100.0%; Score 487; DB 3; Length 214;
Best Local Similarity 100.0%; Pred. No. 8.8e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVKDSPTPTPTDPAHVSTVHGTYAHRDQKSCFIQTLDVVFTRKRGHILELL 60
DB 119 EIVWVKDSPTPTPTDPAHVSTVHGTYAHRDQKSCFIQTLDVVFTRKRGHILELL 178

QY 61 TEVTRMAEALVQEGKARKTNPEIOSTLRKRLYLQ 96
DB 179 TEVTRMAEALVQEGKARKTNPEIOSTLRKRLYLQ 214

RESULT 2

AAV68865
ID AAV68865 standard; protein; 229 AA.

AC AAV68865;

DT 16-MAY-2000 (first entry)

DE Amino acid sequence of a human caspase-like polypeptide.

KM Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
KW keratinisation; wound healing.

OS Homo sapiens.

PN WO200004169-A1.

PD 27-JAN-2000.

PF 12-JUL-1999; 99WO-EP04939.

PR 17-JUL-1998; 98EP-00202422.

PA (VLAAS) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

PI Van De Craen M, Declercq W, Vandenaebelle P, Fiers W;

DR WPI: 2000-182433/16.

DR N-PSDB; AAV60684.

PT New murine and human caspase homologues useful for treating skin related
PT disorders.

PS Claim 2; Page 53-54; 68pp; English.

XX The present sequence represents a human caspase-like polypeptide. The
CC specification also describes a murine caspase-like polypeptide. Caspases
CC are cytosolic aspartate-specific proteinases which play a central role in
CC apoptosis. The polypeptides of the invention are related to human and
CC murine caspase-2 and human caspase-9, and possess all of the typical
CC amino acids involved in catalysis, including the QACRG box, and contain
CC no or only a very short prodomain. mRNA expression of the homologues of
CC the invention is predominant in the skin. The caspase-like polypeptides
CC are useful for treating human or animal diseases, such as skin diseases.
CC They are also useful for screening for compounds that modulate its
CC activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
CC polypeptides and polynucleotides are useful for modulating
CC keratinisation, for diagnosing and treating inappropriate wound healing
XX

SQ Sequence 229 AA;

Query Match 100.0%; Score 487; DB 3; Length 229;
Best Local Similarity 100.0%; Pred. No. 9.7e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVKDSPTPTPTDPAHVSTVHGTYAHRDQKSCFIQTLDVVFTRKRGHILELL 60
DB 134 EIVWVKDSPTPTPTDPAHVSTVHGTYAHRDQKSCFIQTLDVVFTRKRGHILELL 193

QY 61 TEVTRMAEALVQEGKARKTNPEIOSTLRKRLYLQ 96
DB 194 TEVTRMAEALVQEGKARKTNPEIOSTLRKRLYLQ 229

RESULT 3

AAV93214
ID AAV93214 standard; protein; 242 AA.

AC AAV93214;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of a human caspase-14.

KM Caspase-14; cell death specific protease; apoptosis stimulator;
KW apoptosis; AIDS; neurodegenerative disease; ischemic injury.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Region 1..146 /note="large subunit"

FT Active-site 130..134

FT Cleavage-site 146..147

FT Region 147..242 /note="small subunit"

PN WO200028047-A1.

PD 18-MAY-2000.

PF 29-OCT-1999; 99WO-US025523.

PR 06-NOV-1998; 98US-00187789.

PA (UYDE-) UNIV JEFFERSON THOMAS.

PI Alnemri ES, Fernandez-Alnemri T;

DR WPI: 2000-376558/32.

DR N-PSDB; AAA15164.

PT Novel nucleic acids encoding cell death specific protease termed caspase-
PT 14 useful for treating cancers by stimulating apoptosis.

PS Claim 13; Fig 7; 78pp; English.

XX The present sequence represents a human caspase-14 polypeptide. The
CC polypeptide is a cell death specific protease, and is an apoptosis
CC stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
CC -14 antibodies are useful for treating or reducing the severity of
CC pathological conditions associated with increased or decreased levels of
CC apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
CC diseases and ischemic injury are treated by administering anti-caspase-14
CC antibodies. The antibody is useful for determining the presence or the
CC level of caspase-14 in tissue sample and also for the isolation of
CC caspase-14 with apoptotic activity or in screening assay to identify an
CC agent that inhibits heterodimer or heterotetramer formation and
CC therefore, apoptosis
XX

SQ Sequence 242 AA;

Query Match 100.0%; Score 487; DB 3; Length 242;
Best Local Similarity 100.0%; Pred. No. 1e-53;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVKDSPTPTPTDPAHVSTVHGTYAHRDQKSCFIQTLDVVFTRKRGHILELL 60
|||||

Db 147 EIVWVTKDSPQITPTTIDALHYSTVEGYIAYRHDKGSCFIQTLDVDFTRKGHILELL 206
QY 61 TEVTRRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 96
Db 207 TEVTRRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 242

RESULT 4
AAG77980
ID AAG77980 standard; protein; 242 AA.

XX AAG77980;

XX 05-APR-2002 (first entry)

XX Full-length human caspase-14.

XX Human; caspase-14; anti-apoptotic; apoptosis.

XX Homo sapiens.

XX WO200181595-A2.

XX 01-NOV-2001.

XX 27-APR-2001; 2001WO-US013831.

XX 27-APR-2000; 2000US-0199962P.

XX (KNOL) KNOLL GMBH.

XX Mankovich JA;

XX WPI; 2002-041410/05.

XX N-PSDB; AAK98248.

XX Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.

XX Claim 20; Fig 1; 58pp; English.

XX The sequence represents the novel full-length human caspase-14 protein,
CC referred to as "Caspase-14 NEW" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino
CC acid sequence with MSNPRSLER, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein

XX Sequence 242 AA;

XX Query Match 100.0%; Score 487; DB 5; Length 242;

XX Best Local Similarity 100.0%; Pred. No. 1e-53;

XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVTKDSPQITPTTIDALHYSTVEGYIAYRHDKGSCFIQTLDVDFTRKGHILELL 60

Db 147 EIVWVTKDSPQITPTTIDALHYSTVEGYIAYRHDKGSCFIQTLDVDFTRKGHILELL 206

QY 61 TEVTRRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 96

Db 207 TEVTRRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 242

RESULT 5
AAG77984
ID AAG77984 standard; protein; 242 AA.

XX AAG77984;

XX 05-APR-2002 (first entry)

XX Full-length human caspase-14 old.

XX Human; caspase-14; anti-apoptotic; apoptosis.

XX Homo sapiens.

XX WO200181595-A2.

XX 01-NOV-2001.

XX 27-APR-2001; 2001WO-US013831.

XX 27-APR-2000; 2000US-0199962P.

XX (KNOL) KNOLL GMBH.

XX Mankovich JA;

XX WPI; 2002-041410/05.

XX Novel isolated human caspase-14 proteins and nucleic acid sequences,
PT useful for identifying modulators of caspase-14 protein that are useful
PT for modulating apoptosis.

XX Example; Fig 1; 58pp; English.

XX The sequence represents the full-length human caspase-14 protein,
CC referred to as "Caspase-14 OLD" in the specification. The invention
CC relates to a novel isolated human caspase-14 protein comprising an amino
CC acid sequence with MSNPRSLER, at its amino terminus. The caspase-14 of
CC the invention has anti-apoptotic activity. Caspase-14 acts as a modulator
CC of caspase-14 activity. The polypeptide is useful for identifying a
CC compound which is a modulator of human caspase-14 activity, and is also
CC useful for identifying a compound which modulates the interaction of
CC caspase-14 with a target molecule. An antibody to caspase-14 is useful
CC for isolating the protein by standard techniques, and for detecting
CC for isolating the protein by standard techniques, and for detecting
CC caspase-14 to evaluate the abundance and expression pattern. The antibody
CC is also useful for diagnostically monitoring protein levels in a tissue
CC as a part of a clinical testing procedure. The polypeptide is useful as a
CC protease to cleave substrates and for inducing apoptosis in cells, in
CC screening assays, and as a bait protein in a two-hybrid or three-hybrid
CC assay to identify other proteins that interact with human caspase-14
CC protein

XX Sequence 242 AA;

XX Query Match 100.0%; Score 487; DB 5; Length 242;

XX Best Local Similarity 100.0%; Pred. No. 1e-53;

XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVTKDSPQITPTTIDALHYSTVEGYIAYRHDKGSCFIQTLDVDFTRKGHILELL 60

Db 147 EIVWVTKDSPQITPTTIDALHYSTVEGYIAYRHDKGSCFIQTLDVDFTRKGHILELL 206

QY 61 TEVTRRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 96

Db 207 TEVTRRMAAEALVQEGKARKTNPEIOSLTRKRLYLQ 242

RESULT 6
AA568864
ID AA568864 standard; protein; 257 AA.

XX

```

AC AAY68864;
XX
DT 16-MAY-2000 (first entry)
XX DE
XX Amino acid sequence of a murine caspase-like polypeptide.
XX MM Mouse; caspase-like polypeptide; human; caspase; apoptosis; skin disease;
XX KW keratinisation; wound healing.
XX XX
OS Mus musculus.
PN WO200004169-A1.
PD 27-JAN-2000.
XX PF 12-UTL-1999; 99WO-EP004939.
XX PR 17-JUL-1998; 98EP-00202422.
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
PI Van De Craen M, Declercq W, Vandenaebale P, Fiers W;
XX DR WI; 2000-182433/16.
XX DR N-PADB; AAZ60683.
XX PT New murine and human caspase homologues useful for treating skin related
PT disorders.
XX PS
XX PS Claim 1; Page 51-52; 68pp; English.
CC The present sequence represents a murine caspase-like polypeptide. The
CC specification also describes a human caspase-like polypeptide. Caspases
CC are cysteinyl aspartate-specific proteinases which play a central role in
CC apoptosis. The polypeptides of the invention are related to human and
CC murine caspase-2 and human caspase-9, and possess all of the typical
CC amino acids involved in catalysis, including the QACRQ box, and contain
CC not only a very short prodomain. mRNA expression of the homologues of
CC the invention is predominant in the skin. The caspase-like polypeptides
CC are useful for treating human or animal diseases, such as skin diseases.
CC They are also useful for screening for compounds that modulate its
CC activity, i.e. agonists, antagonists, and inhibitors. The caspase-like
CC polypeptides and polymucleotides are useful for modulating
CC keratinisation, for diagnosing and treating inappropriate wound healing
SQ Sequence 257 AA;

Query Match 73.3%; Score 357; DB 3; Length 257;
Best Local Similarity 70.2%; Pred No.5.4e-37;
Matches 66; Conservative 14; Mismatches 14; Indels 0; Gaps 0.

CY 3 VMWIKDSQITPTTYTDALHVSSTVEGYIAYRDQKSGCIQTLLVDVFTRKGHIETLTE 62
|:::|:|||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 164 VAVLNKNPQSIPYTYDTHLYSTVGYSYRDEKSGEIQTLTVDFIHKKSIIELEIE 223
|:::|:|||||||:|||||:|||||:|||||:|||||:|||||:|||||
CY 63 VTRRAEAIVOEGRARKTNPEIGSTIAKKRLYLQ 96
|:::|:|||||||:|||||:|||||:|||||:|||||:|||||
DB 224 ITRLNANTFVMOEGRPKVNEPVOSTLRKKIYLQ 257
|:::|:|||||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
AAW93592 ID AAW93592 standard; protein; 281 AA.
XX AC AAW93592;
XX DT 21-JUN-1999 (first entry)
XX DE Mouse caspase-14 protein.
XX MM
XX Caspase-14; murine; protease; treatment; apoptotic-related disease;
XX KW autoimmune disease; cancer; acquired immunodeficiency syndrome; AIDS;
XX neurodegenerative disease; ischaemic injury; anti-idiotypic antibody;
```

KM	caspase-14 processing activity; epitope; competitor; modulator.
XX	
OS	Mus sp.
FN	WO9910504-A2.
XX	
PD	04-MAR-1999.
XX	
PJ	26-AUG-1998; 98MO-US017715.
XX	
PA	26-AUG-1997; 97US-0056986P.
XX	(IDUN-) IDUN PHARM INC.
PI	Alnemri ES, Fernandes-Alnemri T;
XX	
DR	WPI; 1999-204670/17.
XX	N-PDOB; AAX23515.
PT	Newly isolated polynucleotide encoding a caspase-14 polypeptide - useful
PT	for identifying (ant)agonists that are useful in the diagnosis and
XX	treatment of apoptosis-related diseases.
PS	Claim 4; Fig 1; 59pp; English.
CC	This invention describes a novel murine caspase-14 which has protease
CC	activity. The caspase-14 polypeptide is useful for identifying
CC	(ant)agonists of the polypeptide, where enzyme activity is measured with
CC	a fluorescent substrate (especially DEVD-AMC or YVAD-AMC. Activated
CC	caspase-14 is useful for identifying inhibitors or enhancers of caspase-
CC	14 activity. The compounds identified by both methods form pharmaceutical
CC	compositions for treating apoptotic-related diseases, including
CC	autoimmune disease, cancer, acquired immunodeficiency syndrome (AIDS),
CC	neurodegenerative diseases and ischemic injury. The anti-caspase-14
CC	antibody is useful for measuring the level of caspase-14 in a tissue
CC	sample. An antibody that binds to a caspase-14 polypeptide is useful for
CC	isolating the polypeptide, and an antibody that binds to the large or
CC	small subunit the polypeptide is useful for identifying samples with
CC	caspase-14 processing activity. An antibody that binds to caspase-14
CC	heterodimer or heterotrimer is useful for isolating caspase-14 with
CC	apoptotic activity or in a screening assay to identify (ant)agonists. The
CC	antibodies form kits for such purposes. The anti-caspase-14 antibody is
CC	also useful for preparing anti-idiotypic antibodies, which mimic a
CC	caspase-14 epitope recognized by the anti-caspase-14 antibody. Therefore,
CC	the antibody is useful as a competitor of caspase-14 in reducing the
CC	level of caspase-14 activity, which reduces the level of apoptotic
CC	activity. Oligonucleotides made from the polynucleotides are useful as
CC	polymerase chain reaction (PCR) primers or probes to screen genomic or
CC	cDNA libraries for similar caspase-14 encoding polynucleotides, or for
CC	diagnosis of diseases associated with enhanced or inhibited apoptosis.
CC	The isolated caspase-14 gene permits methods of modulating apoptosis for
CC	the treatment of human diseases
XX	
SQ	Sequence 281 AA;
Query Match	73.3%; Score 357; DB 2; Length 281;
Best local similarity	70.2%; Pval. No. 6.1e-57;
Matches	66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
OY	3 VMVTKSPQTIPTYTDAIAHYSTVEGVIAVRHOKSCSFQIQLVDVFTRKRGIIIELEL 62
DB	183 VAVIKNNPQGIIPYTDLTHIVSVBGLTSRHDHKSGSFIQTITVFIHKKSIIIELEL 242
OY	63 VTIRMMAELVDSGKARKTNPEIQSTRKRRLIYQ 96
DB	243 ITRIMANTEVMDEGKPRKVNPEVOSTLRKKLYIQ 276
RESULT 8	
ID	AAY93213 standard; protein; 281 AA.
XX	AAY93213
GC	AAV93213;


```
XX 04-SEP-2000 (first entry)
XX Amino acid sequence of a murine caspase-14.
DE Caspase-14, cell death specific protease; apoptosis stimulator;
XX apoptosis; AIDS; neurodegenerative disease; ischemic injury.
XX Mus sp.
OS
XX Key
XX Region 1, 156
XX /note="large subunit"
XX Active-site 134, .138
XX Cleavage-site 156, .157
XX Cleavage-site 162, .163
XX Region 163, .257
XX /note="small subunit"
XX WO200028047-A1.
XX 18-MAY-2000.
XX 29-OCT-1999; 99WO-US025523.
XX 06-NOV-1998; 98US-00187789.
XX (UYJE-) UNITV JEFFERSON THOMAS.
XX Alnemri ES, Fernandez-Alnemri T;
XX WPI, 2000-376558/32.
XX N-PSDB; AAA15163.
XX
XX Novel nucleic acids encoding cell death specific protease termed caspase-
PT 14 useful for treating cancers by stimulating apoptosis.
XX
XX Claim 52; Fig 1; 78pp; English.
XX
XX The present sequence represents a murine caspase-14 polypeptide. The
XX polypeptide is a cell death specific protease, and is an apoptosis
XX stimulator. Caspase-14 polynucleotides and polypeptides, and anti-caspase
XX 14 antibodies are useful for treating or reducing the severity of
XX pathological conditions associated with increased or decreased levels of
XX apoptosis. Apoptosis mediated diseases such as AIDS, neurodegenerative
XX diseases and ischemic injury are treated by administering anti-caspase-14
XX antibodies. The antibody is useful for determining the presence or the
XX level of caspase-14 in tissue sample and also for the isolation of
XX caspase-14 with apoptotic activity or in screening assay to identify an
XX agent that inhibits heterodimer or heterotetramer formation and
XX therefore, apoptosis
XX
XX Sequence 281 AA:
SQ
Query Match 73.3%; Score 357; DB 3; Length 281;
Best Local Similarity 70.2%; Pred. No. 6,1e-37;
Matches 66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
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QY 3 VMTYKDSPTPTPTDALTAVYSTVEGYIAYRHDKSGSCFIOTLVDFTRKKGHLELLE 62
DB 183 VANUKNNPQSIPTTDLIAHYSTVEGYLSTRHDKSGSCFIOTLVDFTRKKGHLELLE 242
QY 63 VTRRMAEALVQEGKARKNPETIOSTLRKRLYLQ 96
DB 243 ITRLMANTEVMQEGKARKNPVEVOSTLRKRLYLQ 276
RESULT 9
AAU72882
ID AAU72882 standard; protein; 234 AA.
XX
XX AAU72882;
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DT 26-FEB-2002 (first entry)
DE Human aspartyl protease partial protein sequence #7.
XX
XX Human; protease; PCR primer; cytosolic; immunomodulator; cardiant;
XX vasotropic; antihistamine; analgesic; endocrine; nootropic; tranquiliser;
XX hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;
XX anorectic; antiinflammatory; aspartyl protease; cysteine protease;
XX metalloprotease; serine protease; cancer; haematopoietic; breast; colon;
XX lung; prostate; cervical; brain; ovarian; bladder; kidney; pain;
XX immune-related disease; cardiovascular disease; neuronal disease;
XX migraine; sexual dysfunction; mood disorder; attention disorder;
XX cognition disorder; hypotension; hypertension; psychotic disorder;
XX dyskinesia; metabolic disorder; inflammatory disorder.
XX Homo sapiens.
XX WO200183782-A2.
XX 08-NOV-2001.
XX 04-MAY-2001; 2001WO-US014431.
XX 04-MAY-2000; 2000US-0201879P.
XX (SUGJ-) SUGEN INC.
XX Plowman GD, Whyte D, Sudarsanam S, Manning G, Caenepeel S;
XX Payne V;
XX WPI; 2002-041502/05.
XX N-PSDB; AAS97165.
XX
XX Novel protease polypeptide useful for screening for substances that may
PT be used to treat, e.g., cancers, immune-related diseases, cardiovascular
XX disease, migraine, pain, psychotic and inflammatory disorders.
XX
XX Claim 28; Fig 2A; 232pp; English.
XX
XX The invention relates to an isolated, enriched, or purified protease
XX polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to
XX screen for substances (S) that may modulate its activity. Administering S
XX (which modulates protease activity in vitro) may be used to treat a
XX disease or disorder selected from cancers (e.g., of tissues, of blood or
XX haematopoietic origin, of the breast, colon, lung, prostate, cervical,
XX brain, ovarian, bladder or kidney), immune-related diseases and
XX disorders, cardiovascular disease, brain or neuronal-associated diseases
XX (e.g., central or peripheral nervous system diseases, migraine, pain,
XX sexual dysfunction, mood disorders, attention disorders, cognitive
XX disorders, hypotension, hypertension, psychotic disorders, neurological
XX disorders and dyskinesias), metabolic disorders and inflammatory
XX disorders. (I) may also be useful as a diagnostic tool for a disease or
XX disorder such as those above. AAU72876-AAU72910 represent human protease
XX amino acid sequences of the invention
XX
XX Sequence 234 AA:
SQ
Query Match 40.0%; Score 195; DB 5; Length 234;
Best Local Similarity 48.4%; Pred. No. 2,9e-16;
Matches 44; Conservative 18; Mismatches 25; Indels 4; Gaps 3;
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QY 9 SPOTITPTDALTAVYSTVEGYIAYRHDKSGSCFIOTLVDFTRKKGHLELLEVR 67
DB 144 APSVSHADVQIYVAQGYVVR-DDKSDFIOTLVDFTRKKGHLELLEVR 202
QY 68 AEAELVQEGKARKNPETIOSTLRKRLYLQ 96
DB 203 CEQEVIGPDCDELKAKCLIRSSLRRLCLQ 233
RESULT 10
ABG76499
ID ABG76499 standard; protein; 398 AA.
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Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVWIKSPQITPTPTDALTHYSTVEG 28
147 EIVWIKSPQITPTPTDALTHYSTVEG 174

RESULT 12

AA045325
ID AA045325 standard; protein; 503 AA.

AC AA045325;

DT 25-MAR-2003 (revised)
DT 01-JUL-1994 (first entry)

DE Ced-3 mutant V452.

XX C.elegans; cell death; gene; ced-3; inhibition; human; parasite;
KM interleukin-1beta convertase; ICE; pro-interleukin-1beta; cytokine;
KM inflammatory response; nematode; diagnosis; myocardial infarction;
KM stroke; degenerative disease; traumatic brain injury; hypoxia; pest;
KM pathogenic infection; hair loss; cancer; autoreactive antibody.

OS Caenorhabditis elegans.

XX Key Location/Qualifiers

FT Misc-difference 452
FT /label= V452

PN WO9325694-A1.

XX 23-DEC-1993.

PF 14-JUN-1993; 93WO-US005705.

XX 12-JUN-1992; 92US-00897786.

PR 20-NOV-1992; 92US-00984182.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Horvitz HR, Yuan J, Shaham S;

XX WPI; 1994-007551/01.

PT Agents which affect activity of cell death genes - used to develop drugs
PT for treating conditions characterised by cell death or proliferation.

PS Claim 99; Page 7; 132pp; English.

XX The sequences given in AA045276-328 indicate the positions of possible
CC mutations of the C.elegans cell death gene, ced-3. These mutations occur
CC at conserved amino acid residues of the Ced-3 protein. Fragments of the
CC amino terminal of these proteins act as inhibitors of Ced-3. The ced-3
CC gene has considerable similarity to human interleukin-1beta convertase
CC (ICE), which converts pro-interleukin-1beta to the active cytokine and is
CC involved in inflammatory response in humans. The similarity between the
CC two sequences suggests that inhibitors of ced-3 may also act as
CC inhibitors of ICE. Human ICE and nematode Ced-3 proteins have an overall
CC amino acid similarity of 28%. The ced-3 inhibitors may be used for
CC identifying agents which affect the activity of a gene belonging to the
CC to the ced-3/ICE family of genes and for diagnosis of diseases
CC characterised by cell death. They can also be used to develop drugs for
CC treating conditions characterised by cell deaths such as myocardial
CC infarction, stroke, degenerative disease, traumatic brain injury,
CC hypoxia, pathogenic infection, or hair loss, or drugs for reducing the
CC proliferative capacity or size of a population of cells such as cancerous
CC cells, cells which produce autoreactive antibodies, infected cells, hair
CC follicle cells or cells which are critical to the life of a parasite,
CC pest or recombinant organism. They may also be used in the diagnosis of
CC inflammatory disease. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 503 AA;

Query Match

Best Local Similarity 26.6%; Score 129.5; DB 2; Length 503;
Matches 30; Conservative 19; Mismatches 32; Indels 3; Gaps 2;

Qy 14 PTYDHALVSTVSGYIAVRHDKSGSCIQTLVDFVT--KRGHILELTETVTRMAAE 71
410 PSQADILIRYATTAQYVWRNSARSGSWFIQVCEVFTHADQDVVELITEVKKVASAF 469

Qy 72 LVQEG-KARKTNPETISTARRRLY 94

DB 470 QTSQGSNLIKQMPENTSRLLKKFY 493

RESULT 13

ABB63301
ID ABB63301 standard; protein; 494 AA.

AC ABB63301;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 16695.

XX Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PMD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL07404.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.

PS Disclosure; SEQ ID NO 16695; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

XX Sequence 494 AA;

Query Match

Best Local Similarity 26.2%; Score 127.5; DB 4; Length 494;
Matches 32; Conservative 12; Mismatches 27; Indels 15; Gaps 3;

Qy 16 YTDALHVSSTVSGYIAVRHDKSGSCIQTLVDFVTKRGK--HILELTETVTRMAAE 73
412 HIDMLRAMESTVNGYALRHTQTGSGWFTGSLCDALDRSASEHTADITLITVMEVS----- 466

QY 74 QEGKARKTN-----PEIQSTLRKRLY 94
 Db 467 ---KKRGSDNESWPNVKSTFRQHVY 489

RESULT 14
 AAR45286
 ID AAR45286 standard; protein; 503 AA.

AC AAR45286;

DT 25-MAR-2003 (revised)
 DT 01-JUL-1994 (first entry)

DE Ced-3 mutant D265.

XX C.elegans; cell death; gene; ced-3; inhibition; human; parasite;
 KM interleukin-1beta convertase; ICE; pro-interleukin-1beta; cytokine;
 KM inflammatory response; nematode; diagnosis; myocardial infarction;
 KM stroke; degenerative disease; traumatic brain injury; hypoxia; pest;
 KM pathogenic infection; hair loss; cancer; autoreactive antibody.

XX Caenorhabditis elegans.

OS
 FH Key Location/Qualifiers
 FT Misc-difference 265
 FT /label= D265

PN W09325694-A1.

XX 23-DEC-1993.

XX 14-JUN-1993; 93WO-US005705.

XX 12-JUN-1992; 92US-00897788.
 XX 20-NOV-1992; 92US-00984182.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Horvitz HR, Yuan J, Shaham S;

XX WPI; 1994-007551/01.

PT Agents which affect activity of cell death genes - used to develop drugs
 PT for treating conditions characterised by cell death or proliferation.

PS Claim 93; Page ?; 132pp; English.

XX The sequences given in AAR45276-328 indicate the positions of possible
 CC mutations of the C.elegans cell death gene, ced-3. These mutations occur
 CC at conserved amino acid residues of the Ced-3 protein. Fragments of the
 CC amino terminal of these proteins act as inhibitors of Ced-3. The ced-3
 CC gene has considerable similarity to human interleukin-1beta convertase
 CC (ICE), which converts pro-interleukin-1beta to the active cytokine and is
 CC involved in inflammatory response in humans. The similarity between the
 CC two sequences suggests that inhibitors of ced-3 may also act as
 CC inhibitors of ICE. Human ICE and nematode Ced-3 proteins have an overall
 CC amino acid similarity of 28%. The ced-3 inhibitors may be used for
 CC identifying agents which affect the activity of a gene belonging to the
 CC to the ced-3/ICE family of genes and for diagnosis of diseases
 CC characterised by cell death. They can also be used to develop drugs for
 CC treating conditions characterised by cell deaths such as myocardial
 CC infarction, stroke, degenerative disease, traumatic brain injury,
 CC hypoxia, pathogenic infection, or hair loss; or drugs for reducing the
 CC proliferative capacity or size of a population of cells such as cancerous
 CC cells, cells which produce autoreactive antibodies, infected cells, hair
 CC follicle cells or cells which are critical to the life of a parasite,
 CC pest or recombinant organism. They may also be used in the diagnosis of
 CC inflammatory disease. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 503 AA;

Query Match 26.2%; Score 127.5; DB 2; Length 503;

Best Local Similarity 35.7%; Pred. No. 3.8e-07;
 Matches 30; Conservative 19; Mismatches 32; Indels 3; Gaps 2;

QY 14 PLYTDLHVSTVEGYIAYRHDKSGSCFQTLVDVFT--RRKGHILELTVRRMAEAF 71
 Db 410 PSQADILIRATIAQYVSWNSARGSWFIQAVCEVSTHAKMDVYELTLVKKYASAF 469

QY 72 LVQEG-KARKTPEIQSTLRKRLY 94
 Db 470 QTSQGSNIIKQMEPMTSRLLKFFY 493

RESULT 15
 AAR45304
 ID AAR45304 standard; protein; 503 AA.

AC AAR45304;

DT 25-MAR-2003 (revised)
 DT 01-JUL-1994 (first entry)

DE Ced-3 mutant I321.

XX C.elegans; cell death; gene; ced-3; inhibition; human; parasite;
 KM interleukin-1beta convertase; ICE; pro-interleukin-1beta; cytokine;
 KM inflammatory response; nematode; diagnosis; myocardial infarction;
 KM stroke; degenerative disease; traumatic brain injury; hypoxia; pest;
 KM pathogenic infection; hair loss; cancer; autoreactive antibody.

XX Caenorhabditis elegans.

OS
 FH Key Location/Qualifiers
 FT Misc-difference 321
 FT /label= I321

PN W09325694-A1.

XX 23-DEC-1993.

XX 14-JUN-1993; 93WO-US005705.

XX 12-JUN-1992; 92US-00897788.
 XX 20-NOV-1992; 92US-00984182.

XX (MASI) MASSACHUSETTS INST TECHNOLOGY.

PI Horvitz HR, Yuan J, Shaham S;

XX WPI; 1994-007551/01.

PT Agents which affect activity of cell death genes - used to develop drugs
 PT for treating conditions characterised by cell death or proliferation.

PS Claim 99; Page ?; 132pp; English.

XX The sequences given in AAR45276-328 indicate the positions of possible
 CC mutations of the C.elegans cell death gene, ced-3. These mutations occur
 CC at conserved amino acid residues of the Ced-3 protein. Fragments of the
 CC amino terminal of these proteins act as inhibitors of Ced-3. The ced-3
 CC gene has considerable similarity to human interleukin-1beta convertase
 CC (ICE), which converts pro-interleukin-1beta to the active cytokine and is
 CC involved in inflammatory response in humans. The similarity between the
 CC two sequences suggests that inhibitors of ced-3 may also act as
 CC inhibitors of ICE. Human ICE and nematode Ced-3 proteins have an overall
 CC amino acid similarity of 28%. The ced-3 inhibitors may be used for
 CC identifying agents which affect the activity of a gene belonging to the
 CC to the ced-3/ICE family of genes and for diagnosis of diseases
 CC characterised by cell death. They can also be used to develop drugs for
 CC treating conditions characterised by cell deaths such as myocardial
 CC infarction, stroke, degenerative disease, traumatic brain injury,
 CC hypoxia, pathogenic infection, or hair loss; or drugs for reducing the
 CC proliferative capacity or size of a population of cells such as cancerous
 CC cells, cells which produce autoreactive antibodies, infected cells, hair

CC follicle cells or cells which are critical to the life of a parasite,
CC pest or recombinant organism. They may also be used in the diagnosis of
CC inflammatory disease. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 503 AA;

	Query Match	26.2%	Score 127.5;	DB 2;	Length 503;
	Best Local Similarity	35.7%;	Pred. No. 3.8e-07;		
	Matches	30;	Mismatches	32;	Indels 3; Gaps 2
OY	14	PTYTALHVSSTVEGSIAYVRHDQKSCFIQTIVDFET--KKRGHLLELTTEVTREMAAE	71		
Dd	410	PSQADILIRIATTAQVYSWRNSARSQWFTQAACEVFSTHKAMDVVELTEVNKRVAASAF	469		
OY	72	LVOEG-KARKTNPFIQSTILRRRLY	94		
Dd	470	QTSQSNTLKKQPEPMTSRLLKKFY	493		

Search completed: July 12, 2004, 13:47:48
Job time : 29.562 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:45:17 ; Search time 8.33058 Seconds

(without alignments)
594.928 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242

Sequence: 1 EIVWIKSPOTIPYTDAL.....KARKTNPETQSTLRKRLYLQ 96

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	487	100.0	214	4	US-09-187-789-9
2	487	100.0	242	4	US-09-187-789-5
3	357	73.3	260	4	US-09-187-789-2
4	357	73.3	260	4	US-09-139-600-2
5	204	41.9	53	4	US-09-187-789-65
6	204	41.9	53	4	US-09-139-600-60
7	143	29.4	230	4	US-09-187-789-7
8	123.5	25.4	497	2	US-08-394-189B-6
9	123.5	25.4	497	3	US-08-258-287B-37
10	123.5	25.4	497	3	US-08-368-704C-37
11	123.5	25.4	503	3	US-08-258-287B-36
12	123.5	25.4	503	3	US-08-368-704C-36
13	123.5	25.4	505	2	US-08-394-189B-5
14	123.5	25.4	505	2	PCT-US93-05701-20
15	123.5	25.4	505	5	PCT-US93-05701-5
16	122.5	25.2	503	4	US-09-291-288-12
17	119.5	24.5	489	4	US-08-983-502-9
18	119.5	24.5	489	4	US-09-516-747-9
19	119.5	24.5	489	5	PCT-US96-10521-9
20	119.5	24.5	503	3	US-08-258-287B-2
21	119.5	24.5	503	3	US-08-258-287B-35
22	119.5	24.5	503	3	US-08-368-704C-2
23	119.5	24.5	503	3	US-08-368-704C-35
24	119.5	24.5	503	4	US-08-724-378D-10
25	119.5	24.5	503	5	PCT-US93-05701-19
26	119.5	24.5	503	5	PCT-US93-05705-2
27	119	24.4	277	2	US-08-890-542A-27

28	117.5	24.1	480	5	PCT-US93-05701-21	Sequence 21, Appl
29	117.5	24.1	480	5	PCT-US93-05705-6	Sequence 6, Appl
30	113	23.2	346	2	US-08-618-408B-2	Sequence 2, Appl
31	113	23.2	389	4	US-08-724-378D-2	Sequence 2, Appl
32	113	23.2	389	4	US-08-724-378D-3	Sequence 3, Appl
33	113	23.2	479	1	US-08-665-220-2	Sequence 2, Appl
34	113	23.2	479	3	US-09-291-692-2	Sequence 2, Appl
35	113	23.2	479	4	US-09-561-756-33	Sequence 2, Appl
36	113	23.2	479	4	US-09-227-721-33	Sequence 3, Appl
37	113	23.2	479	4	US-09-954-697-33	Sequence 3, Appl
38	113	23.2	479	4	US-09-089-893A-4	Sequence 4, Appl
39	113	23.2	479	4	US-09-489-155-4	Sequence 4, Appl
40	110	22.6	277	3	US-08-591-605-2	Sequence 2, Appl
41	110	22.6	277	3	US-08-964-308-6	Sequence 6, Appl
42	110	22.6	277	3	US-08-964-308-10	Sequence 10, Appl
43	110	22.6	277	3	US-08-462-969B-4	Sequence 4, Appl
44	110	22.6	277	3	US-08-964-313-6	Sequence 6, Appl
45	110	22.6	277	3	US-08-964-313-10	Sequence 10, Appl

ALIGNMENTS

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RESULT 1
US-09-187-789-9
; Sequence 9, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemuri, Emed S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-187-789-9

Query Match      100.0%; Score 487; DB 4; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.8e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 1 EIVWIKSPOTIPYTDALHYSTVEGYIARHDKSCFTQTLVDVETKRGHLEL 60
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Db 119 EIVWIKSPOTIPYTDALHYSTVEGYIARHDKSCFTQTLVDVETKRGHLEL 178
   |||

Q1 61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
   |||
Db 179 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 214
   |||

RESULT 2
US-09-187-789-5
; Sequence 5, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemuri, Emed S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
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; ORGANISM: Homo sapien
US-09-187-789-5

Query Match
Best Local Similarity 100.0%; Score 487; DB 4; Length 242;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWYKDSPTIPTYDTHLVSTVEGYIAYRHDQKSGCFIQTLDVFTKRKHILL 60
DB 147 EIVWYKDSPTIPTYDTHLVSTVEGYIAYRHDQKSGCFIQTLDVFTKRKHILL 206

QY 61 TEVTRMAEALVOEGKARKTNPEIQSTLRKRLYLQ 96
DB 207 TEVTRMAEALVOEGKARKTNPEIQSTLRKRLYLQ 242

RESULT 3
US-09-187-789-2
; Sequence 2, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-2

Query Match
Best Local Similarity 73.3%; Score 357; DB 4; Length 260;
Matches 66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 3 VVWIKDSPTIPTYDTHLVSTVEGYIAYRHDQKSGCFIQTLDVFTKRKHILL 62
DB 167 VAVLKNPQSIPTIPTYDTHLVSTVEGYISYRDEKSGFIQTLDVFTKRKHILL 226

QY 63 VTRMAEALVOEGKARKTNPEIQSTLRKRLYLQ 96
DB 227 ITRLMANTEVMOEGKPRKVNPEVQSTLRKRLYLQ 260

RESULT 4
US-09-139-600-2
; Sequence 2, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-2

Query Match
Best Local Similarity 73.3%; Score 357; DB 4; Length 260;
Matches 66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;
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```

QY 3 VVWIKDSPTIPTYDTHLVSTVEGYIAYRHDQKSGCFIQTLDVFTKRKHILL 62
DB 167 VAVLKNPQSIPTIPTYDTHLVSTVEGYISYRDEKSGFIQTLDVFTKRKHILL 226

QY 63 VTRMAEALVOEGKARKTNPEIQSTLRKRLYLQ 96
DB 227 ITRLMANTEVMOEGKPRKVNPEVQSTLRKRLYLQ 260

RESULT 5
US-09-187-789-65
; Sequence 65, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434C1
; CURRENT APPLICATION NUMBER: US/09/187,789
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 65
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-187-789-65

Query Match
Best Local Similarity 41.9%; Score 204; DB 4; Length 53;
Matches 36; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 3 VVWIKDSPTIPTYDTHLVSTVEGYIAYRHDQKSGCFIQTLDVFTKRKHILL 53
DB 3 VAVLKNPQSIPTIPTYDTHLVSTVEGYISYRDEKSGFIQTLDVFTKRKHILL 53

RESULT 6
US-09-139-600-60
; Sequence 60, Application US/09139600
; Patent No. 6432628
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434
; CURRENT APPLICATION NUMBER: US/09/139,600
; CURRENT FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 60
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-139-600-60

Query Match
Best Local Similarity 41.9%; Score 204; DB 4; Length 53;
Matches 36; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 3 VVWIKDSPTIPTYDTHLVSTVEGYIAYRHDQKSGCFIQTLDVFTKRKHILL 53
DB 3 VAVLKNPQSIPTIPTYDTHLVSTVEGYISYRDEKSGFIQTLDVFTKRKHILL 53

RESULT 7
US-09-187-789-7
; Sequence 7, Application US/09187789
; Patent No. 6340740
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
```


APPLICANT: Fernandez-Alnemir, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C1
CURRENT APPLICATION NUMBER: US/09/187,789
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapien
US-09-187-789-7

Query Match
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVWIKDSPQITPTDIAHYSTVEG 28
Db 147 EIVWIKDSPQITPTDIAHYSTVEG 174

RESULT 8
US-08-394-189B-6
Sequence 6, Application US/08394189B
Patent No. 5962301
GENERAL INFORMATION:
APPLICANT: Horvitz, Robert
APPLICANT: Yuan, Junying
APPLICANT: Shaham, Shai
TITLE OF INVENTION: RELATEDNESS OF HUMAN INTERLEUKIN-1
TITLE OF INVENTION: BETA CONVERTASE GENE TO A C. ELEGANS CELL DEATH
TITLE OF INVENTION: GENE, INHIBITORY PORTIONS OF THESE GENES AND...
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Filing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,189B
FILING DATE: 24-FEB-2005
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/282,211
FILING DATE: 12-JUL-1994
APPLICATION NUMBER: 07/984,182
FILING DATE: 20-NOV-1992
APPLICATION NUMBER: 07/897,788
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/211001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-394-189B-6

Query Match
Best Local Similarity 25.4%; Score 123.5; DB 2; Length 479;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

Qy 14 PPTDIAHYSTVEGIAVRHDKSCFIQTIVDFT--KRGHILELITETVRMAAE 71
Db 384 PSQADILIAVATTAQYVSRNSARSGSWFIQAVCEVFSLHAKMDVVELITVNVKVAAGF 443

Qy 72 LVQEG-KARKTNPEIQTIRKLY 94
Db 444 QTSQANILKQMPBLTSLRLKKFY 467

RESULT 9
US-08-258-287B-37
Sequence 37, Application US/08258287B
Patent No. 6083735
GENERAL INFORMATION:
APPLICANT: Yuan, Junying
APPLICANT: Miura, Masayuki
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,287B
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/080,850
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0609.3920001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
TELEX: 248636 SSR
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-258-287B-37

Query Match
Best Local Similarity 25.4%; Score 123.5; DB 3; Length 497;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

Qy 14 PPTDIAHYSTVEGIAVRHDKSCFIQTIVDFT--KRGHILELITETVRMAAE 71
Db 402 PSQADILIAVATTAQYVSRNSARSGSWFIQAVCEVFSLHAKMDVVELITVNVKVAAGF 461

Qy 72 LVQEG-KARKTNPEIQTIRKLY 94
Db 462 QTSQANILKQMPBLTSLRLKKFY 485

RESULT 10
US-08-368-704C-37

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; Sequence 37, Application US/08368704C
; Patent No. 6087160
; GENERAL INFORMATION:
; APPLICANT: Yuan, Junying
; APPLICANT: Mura, Masayuki
; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,704C
; FILING DATE: 4-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,287
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,850
; FILING DATE: 24-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3920002
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; TELEX: 248636 SSX
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-08-368-704C-37

Query Match          25.4%; Score 123.5; DB 3; Length 497;
Best Local Similarity 34.5%; Pred. No. 1e-07;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PYTTALHYVSTVEGYIAYRHQKSCFTQTLVDVFT--KRGHITLLETVTRRABAE 71
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 402 PQADLLIYATTAQYVSRNARSQSWFIQAVCEVPSLAKMDVVELTEVKKVACGF 461
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 72 LVQEG-KARKTNPEIQSTLRKRLY 94
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 462 QTSQGNILIKQMPELTSRLTKKEY 485
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-08-258-287B-36
; Sequence 36, Application US/08258287B
; Patent No. 6083735
; GENERAL INFORMATION:
; APPLICANT: Yuan, Junying
; APPLICANT: Mura, Masayuki
; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
```

```
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,287B
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,850
; FILING DATE: 24-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bugalsky, Lawrence B.
; REGISTRATION NUMBER: 35,086
; REFERENCE/DOCKET NUMBER: 0609.3920001
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; TELEX: 248636 SSX
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 503 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; US-08-258-287B-36

Query Match          25.4%; Score 123.5; DB 3; Length 503;
Best Local Similarity 34.5%; Pred. No. 1e-07;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PYTTALHYVSTVEGYIAYRHQKSCFTQTLVDVFT--KRGHITLLETVTRRABAE 71
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 408 PQADLLIYATTAQYVSRNARSQSWFIQAVCEVPSLAKMDVVELTEVKKVACGF 467
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 72 LVQEG-KARKTNPEIQSTLRKRLY 94
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 468 QTSQGNILIKQMPELTSRLTKKEY 491
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-08-368-704C-36
; Sequence 36, Application US/08368704C
; Patent No. 6087160
; GENERAL INFORMATION:
; APPLICANT: Yuan, Junying
; APPLICANT: Mura, Masayuki
; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,704C
; FILING DATE: 4-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,287
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,850
; FILING DATE: 24-JUN-1993
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; LENGTH: 505 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-394-189B-5

Query Match
Best Local Similarity 34.5%; Pred. No. 1e-07;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2.

QY 14 PTYTDALHVSITVEGYIAYNRHDQSGCFIQTLVDVFT--KRGHILELLTEVTRMAEAE 71
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 410 PSQADMILAVATTAQVYSWRNSARGSWFIQAVCEVFSIHAKDMVDVELLTENVKKVACGF 469
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 72 LVQEG-KARKTNPEIOSTLRRLY 94
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 470 QTSQGSNLIKOMPELTSRLKKFY 493
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 14
PCT-US93-05701-20
; Sequence 20, Application PC/TUS9305701
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Cloning and Characterization of Cell Death Genes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Massachusetts Institute of Technology
; STREET: 77 Massachusetts Avenue
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER:
; OPERATING SYSTEM:
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05701
; FILING DATE: 19930614
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 505 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: unsure
; LOCATION: at every Xaa
PCT-US93-05701-20

Query Match
Best Local Similarity 25.4%; Score 123.5; DB 5; Length 505;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2.

QY 14 PTYTDALHVSITVEGYIAYNRHDQSGCFIQTLVDVFT--KRGHILELLTEVTRMAEAE 71
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 410 PSQADMILAVATTAQVYSWRNSARGSWFIQAVCEVFSIHAKDMVDVELLTENVKKVACGF 469
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 72 LVQEG-KARKTNPEIOSTLRRLY 94
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 470 QTSQGSNLIKOMPELTSRLKKFY 493
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 15
PCT-US93-05705-5
; Sequence 5, Application PC/TUS9305705
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Inhibitors of Ced-3 and Related Proteins

```

```

; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Massachusetts Institute of Technology
; STREET: 77 Massachusetts Avenue
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05705
; FILING DATE: 19930714
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 505 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: unsure
; LOCATION: at every Xaa
; PCT-US93-05705-5

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Query Match          25.4%; Score 123.5; DB 5; Length 505;
Best Local Similarity 34.5%; Pred. No. 1e-07;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

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QY 14 PPTDHALHYSTVEGYIARHDQSGSCPIQTLVDVFT--KRGHILELITEVTRMAEAE 71
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Db 410 PQADMILIAVATTAQYVSWNSARGSWFIQAVCEVFSIAKMDVDVEILTEVKKVACGF 469
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
QY 72 LVQEG-KARKTNPEIQSTLRRLY 94
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 470 QTSQGSNIHKQMPELTSRLKKFY 493
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

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Search completed: July 12, 2004, 13:51:58
Job time : 8.33058 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:50:22 ; Search time 23.6033 Seconds

(without alignments)
1268.642 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242

Perfect score: 487
Sequence: 1 EIWVWIKDSPQITPTDALT.....KARKTPEIQTARKRLYLQ 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	487	100.0	214	9	US-09-989-903-9
2	487	100.0	214	14	US-10-068-564-9
3	487	100.0	229	9	US-09-764-803A-4
4	487	100.0	241	15	US-10-114-432-36
5	487	100.0	241	15	US-10-114-432-37
6	487	100.0	242	9	US-09-764-803A-24
7	487	100.0	242	9	US-09-845-028-2
8	487	100.0	242	9	US-09-845-028-9
9	487	100.0	242	9	US-09-989-903-5
10	487	100.0	242	10	US-09-851-873-105
11	487	100.0	242	14	US-10-068-564-5
12	487	100.0	242	15	US-10-114-432-3
13	487	100.0	242	15	US-10-114-432-11
14	487	100.0	242	15	US-10-114-432-13
15	487	100.0	242	15	US-10-114-432-15

16	487	100.0	242	15	US-10-114-432-17	Sequence 17, Appl
17	487	100.0	242	15	US-10-114-432-18	Sequence 18, Appl
18	487	100.0	242	15	US-10-114-432-22	Sequence 22, Appl
19	487	100.0	242	15	US-10-114-432-23	Sequence 23, Appl
20	487	100.0	242	15	US-10-114-432-26	Sequence 26, Appl
21	487	100.0	242	15	US-10-114-432-27	Sequence 27, Appl
22	487	100.0	242	15	US-10-114-432-28	Sequence 28, Appl
23	487	100.0	242	15	US-10-114-432-30	Sequence 30, Appl
24	487	100.0	242	15	US-10-114-432-31	Sequence 31, Appl
25	487	100.0	242	15	US-10-114-432-67	Sequence 67, Appl
26	487	100.0	242	15	US-10-114-432-69	Sequence 69, Appl
27	487	100.0	242	15	US-10-114-432-71	Sequence 71, Appl
28	487	100.0	242	15	US-10-114-432-73	Sequence 73, Appl
29	487	100.0	321	15	US-10-114-432-9	Sequence 9, Appl
30	487	100.0	321	15	US-10-114-432-21	Sequence 21, Appl
31	487	100.0	321	15	US-10-114-432-66	Sequence 66, Appl
32	487	100.0	321	15	US-10-114-432-72	Sequence 72, Appl
33	357	73.3	253	15	US-10-114-432-29	Sequence 29, Appl
34	357	73.3	257	9	US-09-764-803A-2	Sequence 2, Appl
35	357	73.3	260	9	US-09-989-903-2	Sequence 2, Appl
36	357	73.3	260	14	US-10-068-564-2	Sequence 2, Appl
37	204	41.9	53	9	US-09-989-903-65	Sequence 65, Appl
38	204	41.9	53	14	US-10-068-564-65	Sequence 65, Appl
39	195	40.0	234	12	US-10-275-107-42	Sequence 42, Appl
40	195	40.0	398	16	US-10-467-042-3	Sequence 34, Appl
41	143	29.4	174	15	US-10-114-432-34	Sequence 34, Appl
42	143	29.4	230	9	US-09-989-903-7	Sequence 7, Appl
43	143	29.4	230	14	US-10-068-564-7	Sequence 7, Appl
44	143	29.4	230	15	US-10-114-432-5	Sequence 5, Appl
45	143	29.4	230	15	US-10-114-432-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-09-989-903-9
; Sequence 9, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnematl, Enad S.
; TITLE OF INVENTION: Fernandez-Alnemati, Teresa
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; FILE REFERENCE: 480140.434DI
; CURRENT APPLICATION NUMBER: US/09/989,903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-903-9

Query Match 100.0%; Score 487; DB 9; Length 214;
Best Local Similarity 100.0%; Pred. No. 9.6e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIWVWIKDSPQITPTDALT.....KARKTPEIQTARKRLYLQ 60
DB 119 EIWVWIKDSPQITPTDALT.....KARKTPEIQTARKRLYLQ 178
QY 61 TEVTRMAEAEIVQSGKARKTNPEIQSTLRKRLYLQ 96
DB 179 TEVTRMAEAEIVQSGKARKTNPEIQSTLRKRLYLQ 214

RESULT 2
US-10-068-564-9
; Sequence 9, Application US/10068564
; Publication No. US20030040096A1
; GENERAL INFORMATION:

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; APPLICANT: Alnemri, Emed S.
; APPLICANT: Fernandez-Alnemri, Teresa
; TITLE OF INVENTION: CASPASE-1, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434C2
; CURRENT APPLICATION NUMBER: US/10/068,564
; CURRENT FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRF
; ORGANISM: Homo sapien
US-10-068-564-9

Query Match
Best Local Similarity 100.0%; Score 487; DB 14; Length 214;
Best Local Similarity 100.0%; Pred. No. 9,6e-52;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTIKDSPQITPIYTDLAHVYSTVEGYIAVRHDKSGCFIQTLDVDFTKRKGHTLELL 60
DB 119 EIVMTIKDSPQITPIYTDLAHVYSTVEGYIAVRHDKSGCFIQTLDVDFTKRKGHTLELL 178
61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
179 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 214

RESULT 3
US-09-764-803A-4
; Sequence 4, Application US/09764803A
; Patent No. US20020034812A1
; GENERAL INFORMATION:
; APPLICANT: Van de Craen, Marc
; APPLICANT: Declercq, Wim
; APPLICANT: Vandenaebale, Peter
; APPLICANT: Fiers, Walter
; TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
; FILE REFERENCE: 2676-4661US
; CURRENT APPLICATION NUMBER: US/09/764, 803A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: PCT/EP99/04939
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: EP 98202422.6
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 4
; LENGTH: 229
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-764-803A-4

Query Match
Best Local Similarity 100.0%; Score 487; DB 9; Length 229;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTIKDSPQITPIYTDLAHVYSTVEGYIAVRHDKSGCFIQTLDVDFTKRKGHTLELL 60
DB 134 EIVMTIKDSPQITPIYTDLAHVYSTVEGYIAVRHDKSGCFIQTLDVDFTKRKGHTLELL 193
61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
194 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 229

RESULT 4
US-10-114-432-36
; Sequence 36, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.

```

```

; APPLICANT: Fairs, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-2006.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 241
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-10-114-432-36

Query Match
Best Local Similarity 100.0%; Score 487; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTIKDSPQITPIYTDLAHVYSTVEGYIAVRHDKSGCFIQTLDVDFTKRKGHTLELL 60
DB 146 EIVMTIKDSPQITPIYTDLAHVYSTVEGYIAVRHDKSGCFIQTLDVDFTKRKGHTLELL 205
61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
206 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 241

RESULT 5
US-10-114-432-37
; Sequence 37, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Fairs, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-2006.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 241
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-10-114-432-37

Query Match
Best Local Similarity 100.0%; Score 487; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVMTIKDSPQITPIYTDLAHVYSTVEGYIAVRHDKSGCFIQTLDVDFTKRKGHTLELL 60
DB 146 EIVMTIKDSPQITPIYTDLAHVYSTVEGYIAVRHDKSGCFIQTLDVDFTKRKGHTLELL 205
61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
206 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 241

RESULT 6
US-09-764-803A-24

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; Sequence 24, Application US/09764803A
; Patent No. US20020034812A1
; GENERAL INFORMATION:
; APPLICANT: Van de Craen, Marc
; APPLICANT: Declercq, Wim
; APPLICANT: Vandenabeele, Peter
; APPLICANT: Fiers, Walter
; TITLE OF INVENTION: NEW CASPASE HOMOLOGUE
; FILE REFERENCE: 2676-4661US
; CURRENT APPLICATION NUMBER: US/09/764, 803A
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: PCT/EP99/04939
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: EP 98202422.6
; PRIOR FILING DATE: 1999-07-17
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 242
; SEQ ID NO 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: misc. feature
; OTHER INFORMATION: Description of Artificial Sequence: predicted (genscan program)
; US-09-764-803A-24
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Query Match          100.0%; Score 487; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EIVWVTKDSPQTIPTTALHVSSTVEGYIAVRHDKSGCFIQTLDVDFTKRKHILELL 60
DB 147 EIVWVTKDSPQTIPTTALHVSSTVEGYIAVRHDKSGCFIQTLDVDFTKRKHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 242
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RESULT 7
US-09-845-028-2
; Sequence 2, Application US/09845028
; Patent No. US20020081705A1
; GENERAL INFORMATION:
; APPLICANT: Mankovich, John
; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
; FILE REFERENCE: BBI-111
; CURRENT APPLICATION NUMBER: US/09/845, 028
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199, 962
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-845-028-2
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Query Match          100.0%; Score 487; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EIVWVTKDSPQTIPTTALHVSSTVEGYIAVRHDKSGCFIQTLDVDFTKRKHILELL 60
DB 147 EIVWVTKDSPQTIPTTALHVSSTVEGYIAVRHDKSGCFIQTLDVDFTKRKHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 242
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RESULT 8
US-09-845-028-9
; Sequence 9, Application US/09845028
; Patent No. US20020081705A1
; GENERAL INFORMATION:
; APPLICANT: Mankovich, John
; TITLE OF INVENTION: HUMAN CASPASE-14 COMPOSITIONS
; FILE REFERENCE: BBI-111
; CURRENT APPLICATION NUMBER: US/09/845, 028
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/199, 962
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-845-028-9
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Query Match          100.0%; Score 487; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EIVWVTKDSPQTIPTTALHVSSTVEGYIAVRHDKSGCFIQTLDVDFTKRKHILELL 60
DB 147 EIVWVTKDSPQTIPTTALHVSSTVEGYIAVRHDKSGCFIQTLDVDFTKRKHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 242
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RESULT 9
US-09-989-903-5
; Sequence 5, Application US/09989903
; Patent No. US20020146804A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: CASPASE-14, AN APOPTOTIC PROTEASE, NUCLEIC ACID ENCODING
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 480140.434D1
; CURRENT APPLICATION NUMBER: US/09/989, 903
; CURRENT FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-989-903-5
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Query Match          100.0%; Score 487; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 EIVWVTKDSPQTIPTTALHVSSTVEGYIAVRHDKSGCFIQTLDVDFTKRKHILELL 60
DB 147 EIVWVTKDSPQTIPTTALHVSSTVEGYIAVRHDKSGCFIQTLDVDFTKRKHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIQSTLRKRLYIQ 242
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RESULT 10
US-09-851-873-105
; Sequence 105, Application US/09851873
; Publication No. US20030165488A1
; GENERAL INFORMATION:
; APPLICANT: Kleczien, Rolf F
; APPLICANT: Reardon, Ilene M
```

APPLICANT: Weiland, Katherine L
TITLE OF INVENTION: HUMAN CASPASE-12 MATERIALS AND METHODS
FILE REFERENCE: 28341/00233
CURRENT APPLICATION NUMBER: US/09/851,873
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapiens
US-09-851-873-105

Query Match
Best Local Similarity 100.0%; Score 487; DB 10; Length 242;
Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWIKDSPQITPTTDLAHVSTVEGYIAYRHDKGSCFIQTLLVDVFTKRGHILELL 60
DB 147 EIVWIKDSPQITPTTDLAHVSTVEGYIAYRHDKGSCFIQTLLVDVFTKRGHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 242

RESULT 11
US-10-068-564-5
Sequence 5, Application US/10068564
Publication No. US20030040096A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: CASPASE-14, AN APOTOTIC PROTEASE, NUCLEIC ACID ENCODING
FILE REFERENCE: 480140.434C2
CURRENT APPLICATION NUMBER: US/10/068,564
CURRENT FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 242
TYPE: PRT
ORGANISM: Homo sapien
US-10-068-564-5

Query Match
Best Local Similarity 100.0%; Score 487; DB 14; Length 242;
Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWIKDSPQITPTTDLAHVSTVEGYIAYRHDKGSCFIQTLLVDVFTKRGHILELL 60
DB 147 EIVWIKDSPQITPTTDLAHVSTVEGYIAYRHDKGSCFIQTLLVDVFTKRGHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 242

RESULT 12
US-10-114-432-3
Sequence 3, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-3

Query Match
Best Local Similarity 100.0%; Score 487; DB 15; Length 242;
Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWIKDSPQITPTTDLAHVSTVEGYIAYRHDKGSCFIQTLLVDVFTKRGHILELL 60
DB 147 EIVWIKDSPQITPTTDLAHVSTVEGYIAYRHDKGSCFIQTLLVDVFTKRGHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 242

RESULT 13
US-10-114-432-11
Sequence 11, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Robert K.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 213P1F11 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20066.00
CURRENT APPLICATION NUMBER: US/10/114,432
CURRENT FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 242
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-114-432-11

Query Match
Best Local Similarity 100.0%; Score 487; DB 15; Length 242;
Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWIKDSPQITPTTDLAHVSTVEGYIAYRHDKGSCFIQTLLVDVFTKRGHILELL 60
DB 147 EIVWIKDSPQITPTTDLAHVSTVEGYIAYRHDKGSCFIQTLLVDVFTKRGHILELL 206
QY 61 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 96
DB 207 TEVTRMAEAEIVQEGKARKTNPEIOSTLRKRLYLQ 242

RESULT 14
US-10-114-432-13
Sequence 13, Application US/10114432
Publication No. US20040019915A1
GENERAL INFORMATION:
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Farris, Mary
APPLICANT: Hubert, Rene S.


```
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-13
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Query Match          100.0%; Score 487; DB 15; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      147 EIVWYIKDSPQTIPTYTALAHVYSTVEGYIAVRHDQKSCFTQTLVDVFTKRKHILLEL 206
QY      61  TEVTRMAEALVQEGKARKTNPEIQSTIRKRLYLQ 96
DB      207 TEVTRMAEALVQEGKARKTNPEIQSTIRKRLYLQ 242
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RESULT 15
US-10-114-432-15
; Sequence 15, Application US/10114432
; Publication No. US20040019915A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Robert K.
; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobivits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 213P11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20066.00
; CURRENT APPLICATION NUMBER: US/10/114,432
; CURRENT FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-114-432-15
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Query Match          100.0%; Score 487; DB 15; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  EIVWYIKDSPQTIPTYTALAHVYSTVEGYIAVRHDQKSCFTQTLVDVFTKRKHILLEL 60
DB      147 EIVWYIKDSPQTIPTYTALAHVYSTVEGYIAVRHDQKSCFTQTLVDVFTKRKHILLEL 206
QY      61  TEVTRMAEALVQEGKARKTNPEIQSTIRKRLYLQ 96
DB      207 TEVTRMAEALVQEGKARKTNPEIQSTIRKRLYLQ 242
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Search completed: July 12, 2004, 14:04:01
Job time : 24.6033 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:44:06 ; Search time 6.94215 Seconds

(without alignments)
1330.191 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242
Perfect score: 487
Sequence: 1 EIVWIKDSPQTIPTPTDAL.....KARKTNPEIQSTLRKRLYLQ 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query length	ID	Description
1	487	100.0	242	UC7517	caspace-14/a - hum
2	127.5	26.2	488	TI1385	hypothetical prote
3	123	25.3	277	UC5410	CPB2 protein - mo
4	122.5	25.2	503	A49429	interleukin-1 beta
5	122	25.1	277	S64710	cysteine proteinas
6	115	23.6	536	T43633	caspace-related pr
7	109	22.4	277	A55315	hypothetical prote
8	105.5	21.7	642	T27021	hypothetical prote
9	104	21.4	495	T20038	caspace-2 - rat
10	101.5	20.8	452	UC6507	hypothetical prote
11	101.5	20.8	826	T43638	caspace-related pr
12	99	20.3	454	UC7123	caspace-9 long cna
13	98.5	20.2	435	A54821	apoptosis regulato
14	98	20.1	416	G02635	ICB-LAP6 - human
15	97.5	20.0	139	T43642	caspace protein 3
16	91	18.7	394	T26968	hypothetical prote
17	86	17.7	212	T7437	cysteine proteinas
18	78.5	16.1	505	S39520	H+-transporting tw
19	73.5	15.1	526	T21811	hypothetical prote
20	71.5	14.7	407	UC851	polyketide synthas
21	71.5	14.7	407	T17222	Pms protein - huma
22	71.5	14.3	366	T03907	TGF-beta-related p
23	69.5	14.3	366	F71365	probable DNA polym
24	69.5	14.3	1165	A70423	valine-tRNA ligase
25	69	14.2	473	B72274	hypothetical prote
26	68	14.0	317	A75008	udp-glucose 4-epim
27	68	14.0	896	S43074	epidermal growth f
28	67.5	13.9	164	S56476	hypothetical prote

30	67.5	13.9	226	2	TI6991	ribonuclease (EC 3
31	67.5	13.9	493	1	SI1663	NADH2 dehydrogenas
32	67	13.8	260	2	D27793	methyl coenzyme M
33	67	13.8	342	2	A37952	probable thyroid h
34	67	13.8	352	2	G71328	probable flagellar
35	67	13.8	411	2	A82566	membrane fusion pr
36	67	13.8	418	1	TYX17A	thyroid hormone re
37	67	13.8	423	2	F64690	type IIS restricti
38	67	13.8	447	2	T05003	hypothetical prote
39	67	13.8	1599	2	TI5854	hypothetical prote
40	66.5	13.7	279	2	A86707	transposase of IS9
41	66.5	13.7	2175	2	A59255	myosin VIIa, long
42	66	13.6	391	2	I51097	thyroid hormone re
43	66	13.6	571	2	S24482	conditioned medium
44	66	13.6	571	2	A42138	conditioned medium
45	65.5	13.4	448	2	E82901	RNA polymerase sig

ALIGNMENTS

```
RESULT 1
UC7517
caspace-14/a - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
R:Biochem. Biophys. Res. Commun. 277, 655-659, 2000
A:Title: Caspace-14: Analysis of gene structure and mRNA expression during keratinocyte
A:Reference number: UC7517; MUID:20517231; PMID:11062009
A:Contents: Epidermal keratinocytes
A:Accession: UC7517
A:Molecule type: mRNA
A:Residues: 1-242 <ECK>
A:Cross-references: GB:AF097874
C:Comment: This enzyme accumulates during keratinocyte differentiation and is activated
C:Genetics:
A:Gene: casp-14/a
A:Map position: 19p13.1
A:Introns: 9/3; 59/3; 135/1; 174/1; 208/3
C:Keywords: differentiation

Query Match      100.0%; Score 487; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWIKDSPQTIPTPTDALHVSVFEGYIAVRHDKSGCFQTLDVFTKRKGHILEL 60
    |||
Db 147 EIVWIKDSPQTIPTPTDALHVSVFEGYIAVRHDKSGCFQTLDVFTKRKGHILEL 206
    |||

QY 61 TEVTRMAEALVQEGKARKTNPEIQSTLRKRLYLQ 96
    |||
Db 207 TEVTRMAEALVQEGKARKTNPEIQSTLRKRLYLQ 242
    |||

RESULT 2
TI3385
hypothetical protein 11502.9 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
R:Salles, C.; Valenti, P.; Darlamietsou, A.; Henderson, N.; Campbell, L.; Glover, D.
A:Submitted to the EMBL Data Library, May 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17665
A:Accession: TI3385
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-488 <CAR>
A:Cross-references: EMBL:AL031581; NID:e1320978; PID:e1331441; PIDN:CAA20893.1
A:Genetics:
A:Cross-references: FlyBase:FBgn0020381
```


A:Map position: 2

C:Function:

A:Description: probably acts in proteolytic cascades to regulate processes such as proga

C:Keywords: cysteine proteinase; hydrolase

Query Match 23.6%; Score 115; DB 2; Length 536;

Best Local Similarity 31.9%; Pred. No. 0.00042; Mismatches 37; Indels 4; Gaps 3;

Matches 30; Conservative 23; Mismatches 37; Indels 4; Gaps 3;

QY 3 WVAIDSDQPTPTV-TDALHYSTVEGYIARRHDKGSCFIQTLVDVFTK--RKGHILELTVETRRMA-E 59

Db 436 LMSRIMPGTFTSLNADVILSFTTDGFTSYRDEEGTMYIKSMCKVFENKSKTMHLIDI 495

QY 60 LTVETRR-MAEALVOEGKAKTNPFIQSTLRKR 92

Db 496 LTEIGRNVVTKYENVQGNVVLKQAPFILLRLTKQ 529

RESULT 7

A55315

cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

N:Alternate names: cysteine proteinase CPP32

C:Species: Homo sapiens (man)

C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000

C/Accession: A55315; S58899; I39005

R/Fernandes-Alnemri, T.; Litwack, G.; Alnemri, E.S.

J. Biol. Chem. 269, 30761-30764, 1994

A/Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elegans

A/Reference number: A55315; MUID:95074098; PMID:7983002

A/Accession: A55315

A>Status: preliminary

A:Molecule type: mRNA

A/Residues: 1-277 <FEER>

A/Cross-references: GB:U13737; NID:9561665; PIDN:AAA65015.1; PID:9561666

A/Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammalian

A/Reference number: S58899; MUID:95319529; PMID:7596430

A/Accession: S58899

A:Molecule type: protein

A/Residues: 29-46;176-189, 'E',191-193 <NIG>

R/Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poitrier,

Cell 81, 801-809, 1995

A/Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable protease

A/Reference number: A56924; MUID:95292347; PMID:7774019

A/Accession: I39005

A>Status: preliminary

A:Molecule type: mRNA

A/Residues: 1-189, 'E',191-277 <RES>

A/Cross-references: EMBL:U26943; NID:9857568; PIDN:AAA74929.1; PID:9857569

C:Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte

Query Match 22.4%; Score 109; DB 2; Length 277;

Best Local Similarity 37.5%; Pred. No. 0.00085; Mismatches 36; Indels 6; Gaps 3;

Matches 33; Conservative 13; Mismatches 36; Indels 6; Gaps 3;

QY 13 IFTYDALHYSTVEGYIARRHDKGSCFIQTLVDVFTK--RKGHILELTVETRRMA-E 69

Db 187 IIPDADFLYAKSTAPGYWMRNKDSWFIQSCAMLYKQADLEFMILITRNKRVAIE 246

QY 70 AEIVQ--EGKARKTNPFIQSTLRKRLY 94

Db 247 FESFSFDATFAKQIPICIIVSMILKELY 274

RESULT 8

T27021

hypothetical protein Y48E1B.13 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T27021

R/McMurray, A.

submitted to the EMBL Data Library, March 1997

A/Reference number: Z20299

A/Accession: T27021

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A/Residues: 1-642 <MIL>

A/Cross-references: EMBL:Z93393; PIDN:CAB07698.1; GSPDB:GN00020; CESP:Y48E1B.13

A/Experimental source: clone Y48E1B

C/Genetics:

A/Map position: 2

A/Introns: 79/3; 122/3; 239/2; 286/3; 333/1; 417/3; 487/1; 589/1; 609/3

Query Match 21.7%; Score 105.5; DB 2; Length 642;

Best Local Similarity 32.5%; Pred. No. 0.005; Mismatches 27; Indels 7; Gaps 3;

Matches 26; Conservative 20; Mismatches 27; Indels 7; Gaps 3;

QY 15 TYT---DALHYSTVEGYIARRHDKGSCFIQTLVDVFTK--RKGHILELTVETRR-M 67

Db 500 TFTSLNADVILSFTTDGFTSYRDEAGTWIKSMCKVFENKSKTMHLIDITETGRNVV 559

QY 68 AEALVOEGKAKTNPFIQSTLRKR 87

Db 560 TKENVQGNVVLKQAPFVGS 579

RESULT 9

T20038

hypothetical protein C48D1.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T20038

R/Burton, J.

submitted to the EMBL Data Library, October 1996

A/Reference number: Z19214

A/Accession: T20038

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A/Residues: 1-495 <WIL>

A/Cross-references: EMBL:Z81049; PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2

A/Experimental source: clone C48D1

C/Genetics:

A/Map position: 4

A/Introns: 44/3; 93/2; 178/1; 288/3; 360/1; 402/3; 466/1

Query Match 21.4%; Score 104; DB 2; Length 495;

Best Local Similarity 36.8%; Pred. No. 0.0054; Mismatches 18; Indels 2; Gaps 1;

Matches 21; Conservative 16; Mismatches 18; Indels 2; Gaps 1;

QY 14 PYYTDLHYSTVEGYIARRHDKGSCFIQTLVDVFTK--KRGHILELTVETRRMA 68

Db 409 PSQADILYATTAQYVSWRNARGSMWFIQVCEVSTHAKMDVVELITEVKKVA 465

RESULT 10

JC6507

caesape-2 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C/Accession: JC6507

R/Rato, N.; Milligan, C.E.; Uchiyama, Y.; Oppenheim, R.W.

Gene 202, 127-132, 1997

A/Title: Cloning and expression of the cDNA encoding rat caesape-2.

A/Reference number: JC6507; MUID:98087427; PMID:9427555

A/Accession: JC6507

A>Status: preliminary

A:Molecule type: mRNA

A/Residues: 1-452 <SAT>

A/Cross-references: GB:U77933; NID:92769705; PIDN:AAB96379.1; PID:92769706

Query Match 20.8%; Score 101.5; DB 2; Length 452;

Best Local Similarity 31.5%; Pred. No. 0.0089; Mismatches 27; Indels 7; Gaps 3;

Matches 26; Conservative 20; Mismatches 27; Indels 7; Gaps 3;

Matches 29; Conservative 21; Mismatches 29; Indels 13; Gaps 3;

QY 13 IPTYTDALHYSTVEGYIARHDKGSCFIQTLDVPTKR--KGHILELLEVTYRMAEA 70
 Db 358 LPTPSDMIQGYACLGKMAARNTKRGSWYTEALQVFSRACDMHVDMLVKYNALIKE- 416

QY 71 ELVQEGKARKTN-----PEIQSTLRKRLYL 95
 Db 417 ---REGVAPGTEFHRCKEMSEYCYSTLCQQLYL 445

RESULT 11
 T43638
 caspase-related proteinase 2A (EC 3.4.22.-) - Caenorhabditis elegans
 N:Contains: caspase 2B
 C:Species: Caenorhabditis elegans
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C/Accession: T43638; T43639
 R/Shanam, S.
 J. Biol. Chem. 273, 35109-35117, 1998
 A>Title: Identification of multiple Caenorhabditis elegans caspases and their potential
 A/Reference number: Z22587, MUID:99074291, PMID:9857046
 A/Accession: T43638
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-826 <SHA>
 A/Cross-references: EMBL:AF088288; NID:g4063373; PIDN:AAC98295.1; PID:g4063374
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 564-826 <SH2>
 A/Cross-references: EMBL:AF088289; NID:g4063375; PIDN:AAC98296.1; PID:g4063376
 C/Genetics:
 A/Gene: csp-2
 A/Map position: 4
 C/Keywords: cysteine proteinase; hydrolase

Query Match 20.8%; Score 101.5; DB 2; Length 826;
 Best Local Similarity 32.6%; Pred. No. 0.017;
 Matches 29; Conservative 17; Mismatches 40; Indels 3; Gaps 2;

QY 9 SPQITFTYTDALHYSTVEGYIARHDKGSCFIQTLDVPTKR--RKGHILELLEVTYR 66
 Db 735 SHQTSSQADLLVFSFSTSGFLSFDEFTKGTWYICLAVYIIENADTHLADLMETNR 794

QY 67 MAEA-ELVQEGKARKTNPEIQSTLRKRLYL 94
 Db 795 VVEKYHADKVVIVCKQAPFWSRFTKQLP 823

RESULT 12
 JC7123
 caspase-9 long chain - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
 C/Accession: JC7123
 R/Fujita, E.; Ujino, A.; Matsumaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
 Biochem. Biophys. Res. Commun. 264, 550-555, 1999
 A>Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9.
 A/Reference number: JC7123; MUID:20001956; PMID:10529400
 A/Accession: JC7123
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-454 <FUU>
 A/Cross-references: DBJ:AB019600; NID:g6440941; PID:g6440942

Query Match 20.3%; Score 99; DB 2; Length 454;
 Best Local Similarity 30.8%; Pred. No. 0.016;
 Matches 28; Conservative 18; Mismatches 37; Indels 8; Gaps 2;

QY 8 DSPQITFTYTDALHYSTVEGYIARHDKGSCFIQTLDVPTKR--RKGHILELLEVTYR 65
 Db 368 DAVSSLPISDILVSYSTFPGFVSWRDKKSGSWYTELTDGILFQWARSDELQSLILRV-- 425

QY 66 RMAEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
 Db 426 ---ANAVSEKGTYYKOIPGCENFLRKLLPFK 452

RESULT 13
 A54821
 apoptosis regulator ICH-1, stimulatory form L - human
 C/Species: Homo sapiens (man)
 C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C/Accession: A54821
 R/Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J.
 Cell 78, 739-750, 1994
 A>Title: ICH-1, an Ice/ced-3-related gene, encodes both positive and negative regulators
 A/Reference number: A54821; MUID:94373811; PMID:8087842
 A/Accession: A54821
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-435 <MAN>
 A/Cross-references: GB:U13021; NID:9537291; PID:9537292
 C/Keywords: alternative splicing; apoptosis

Query Match 20.2%; Score 98.5; DB 2; Length 435;
 Best Local Similarity 30.4%; Pred. No. 0.017;
 Matches 28; Conservative 21; Mismatches 30; Indels 13; Gaps 3;

QY 13 IPTYTDALHYSTVEGYIARHDKGSCFIQTLDVPTKR--KGHILELLEVTYRMAEA 70
 Db 341 LPTPSDMIQGYACLGKMAARNTKRGSWYTEALQVFSRACDMHVDMLVKYNALIKD- 399

QY 71 ELVQEGKARKTN-----PEIQSTLRKRLYL 95
 Db 400 ---REGVAPGTEFHRCKEMSEYCYSTLCRHLYL 428

RESULT 14
 G02635
 ICE-LAP6 - human
 C/Species: Homo sapiens (man)
 C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
 C/Accession: G02635
 R/Huan, H.; Orth, K.; Chinaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, W.W.; Dixit,
 submitted to the EMBL Data Library, April 1996
 A/Reference number: H01513
 A/Accession: G02635
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-416 <DUA>
 A/Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027

Query Match 20.1%; Score 98; DB 2; Length 416;
 Best Local Similarity 31.5%; Pred. No. 0.019;
 Matches 28; Conservative 22; Mismatches 35; Indels 4; Gaps 3;

QY 8 DSPQITFTYTDALHYSTVEGYIARHDKGSCFIQTLDVPTKRKGHILELLEVTYRMA 67
 Db 330 DAISSLPISDILVSYSTFPGFVSWRDKKSGSWYTELTDLF-EGWAH-SEDLQSLILRV 387

QY 68 AEAEIVQEGKARKTNPEIQSTLRKRLYLQ 96
 Db 388 ANAVSVK--GIYKQMPGCGCNFLRKLLPFK 414

RESULT 15
 T43642
 caspase protein 3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
 C/Accession: T43642
 R/Shanam, S.
 J. Biol. Chem. 273, 35109-35117, 1998
 A>Title: Identification of multiple Caenorhabditis elegans caspases and their potential

A:Reference number: Z22587; MWID:99074291; PMID:9857046
 A:Accession: T43642
 A:Status: preliminary; translated from GB/EMBL/DDDD
 A:Molecule type: mRNA
 A:Residues: 1-139 <SHA>
 A:Cross-references: EMBL:AF088290; NID:g4063377; PIND:AAC98297.1; PID:g4063378
 C:Genetics:
 A:Gene: csp-3
 A:Map position: 1

Query Match	20.0%	Score	97.5	DB 2	Length	139			
Best Local Similarity	31.5%	Pred	No. 0.0062						
Matches	28	Conservative	18	Mismatches	40	Indels	3	Gaps	2

[illegible]

Search completed: July 12, 2004, 13:51:03
Job time : 7.94215 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:40:11 ; Search time 4.76033 Seconds

(without alignments)
1050.081 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242

Perfect score: 487
Sequence: 1 EIVWIKDSPQITPTDYL.....KARKTNPETOSTLRRLYLQ 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	487	100.0	242	1	ICB6_HUMAN P31944 homo sapien
2	357	73.3	257	1	ICB6_MOUSE O89094 mus musculu
3	123	25.3	277	1	ICB3_MOUSE P70677 mus musculu
4	122.5	25.2	503	1	CEB3_CAEL P42573 caenorhabdi
5	122	25.1	277	1	ICB3_CRILLO Q60431 cricetulus
6	120	24.6	277	1	ICB3_RAT P55213 rattus norv
7	119.5	24.5	496	1	P45436 caenorhabdi
8	114	23.4	303	1	ICB7_MOUSE P97664 mus musculu
9	109	22.4	277	1	ICB3_HUMAN P42574 homo sapien
10	107	22.0	282	1	ICB3_XENLA P53866 xenopus lae
11	107	22.0	303	1	ICB7_HUMAN P55210 homo sapien
12	107	22.0	303	1	ICB7_MESAU P55214 mesocricetu
13	104.5	21.5	424	1	ICB2_CHICK Q98943 gallus gall
14	101.5	20.8	435	1	ICB2_MOUSE P29594 mus musculu
15	101	20.7	276	1	ICB6_MOUSE O08738 mus musculu
16	101	20.7	293	1	ICB6_HUMAN P55212 homo sapien
17	98.5	20.2	435	1	ICB3_HUMAN P42575 homo sapien
18	98	20.1	416	1	ICB3_HUMAN P55211 homo sapien
19	97.5	20.0	299	1	ICB1_SPROF P89116 spodoptera
20	96	19.7	323	1	ICB1_DROME O02002 drosophila
21	95.5	19.6	479	1	ICB8_HUMAN O14790 h caspase-8
22	92	18.9	339	1	ICB6_MOUSE O01382 drosophila
23	86.5	17.8	521	1	ICB6_HUMAN O92851 homo sapien
24	78.5	16.1	505	1	ATPA_GALST P35009 galdiera s
25	75.5	15.5	480	1	ICB8_MOUSE O89110 mus musculu
26	73.5	15.1	373	1	ICB4_MOUSE P70143 mus musculu
27	71	14.6	874	1	SVY_STRCO O06851 streptomyce
28	69.5	14.3	997	1	DPO1_TREPA P74933 treponema p
29	69.5	14.3	1165	1	SVY_AQUAE O67411 aquifex aeo
30	69	14.2	395	1	THB_PAROL Q91279 paralichthy
31	69	14.2	2294	1	YCF2_ARATH P56786 arabidopsis
32	68.5	14.1	1222	1	PNP5_HUMAN O15155 homo sapien
33	68	14.0	418	1	THAB_XENLA P18115 xenopus lae

34	68	14.0	896	1	EP15_HUMAN P42566 homo sapien
35	67.5	13.9	197	1	YRGJ_ECOLI P39334 escherichia
36	67.5	13.9	404	1	ILBC_CANFA Q9mzv7 canis famli
37	67.5	13.9	493	1	NIBM_NEUCR P24917 neurospora
38	67	13.8	260	1	MCRG_METVA P07963 methanococc
39	67	13.8	418	1	THA_RANCA Q02777 rana catesb
40	66.5	13.7	382	1	ICB6_XENLA P55867 xenopus lae
41	66.5	13.7	2215	1	MY7A_HUMAN Q13402 homo sapien
42	66	13.6	391	1	THAB_PAROL Q91242 paralichthy
43	66	13.6	571	1	CMF_DICDI P34090 dictyostell
44	65	13.3	358	1	FLHB_HELPV Q92173 helicobacte
45	65	13.3	373	1	THB_RANCA Q02965 rana catesb

ALIGNMENTS

```

RESULT 1
ICB6_HUMAN STANDARD; PRT; 242 AA.
AC P31944; O95823;
DT 01-JUL-1993 (Rel. 26, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14).
GN CASP14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22168928; PubMed=12181750;
RA Pistrutto G., Jost M., Srinivasula S.M., Baffa R., Poyet J.-L.,
RA Kari C., Lazebnik Y., Rodeck U., Alnemri E.S.;
RT "Expression and transcriptional regulation of caspase-14 in simple
RT and complex epithelia.";
RL Cell Death Differ. 9:995-1006(2002).
[2]
RP SEQUENCE OF 68-74; 137-147 AND 154-162.
RX TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
CC -!- FUNCTION: May be involved in the death receptor and granzyme B
CC apoptotic pathways. May function as a downstream signal transducer
CC of cell death.
CC -!- SUBUNIT: May dimerize with large prodomain caspases.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC
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CC
CC EMBL; AF097874; AAD16173.1; -.
CC PIR; JC7517; JC7517.
CC HSSP; P29466; IICE.
CC Aarhus/cheat-2DPAGE; 6109; IEF.
CC MEROPS; C14.018; -.
CC Genew; HGNC:1502; CASP14.
CC MIM; 605848; -.
CC GO; GO:0004199; F:caspase activity; TAS.
CC GO; GO:0008544; P:epidermal differentiation; TAS.
CC InterPro; IPR002138; ICE_p10.

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DR InterPro: IPR001309; ICE p20.
DR InterPro: IPR002398; Peptidase C14.
DR Pfam: PF00656; Peptidase C14; 1.
DR PRINTS: PR00376; ILICENZTME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE: PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Apoptosis; Zymogen.
KM PROPP 1 ?
FT CHAIN 1 146 CASPASE-14 SUBUNIT 1 (POTENTIAL).
FT CHAIN 2 242 CASPASE-14 SUBUNIT 2 (POTENTIAL).
FT ACT SITE 89 89 BY SIMILARITY.
FT ACT SITE 132 132 BY SIMILARITY.
SQ SEQUENCE 242 AA; 27679 MW; E539B7E8D808A2 CRC64;

Query Match 100.0%; Score 487; DB 1; Length 242;
Best Local Similarity 100.0%; Pred. No. 3.8e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVWVKDSPTPTPTDHALHVSTVEGYIAYRHDKGSCFIQTLDVFTKRKGIIEILL 60
DB 147 EIVWVKDSPTPTPTDHALHVSTVEGYIAYRHDKGSCFIQTLDVFTKRKGIIEILL 206
QY 61 TEVTRMAEALVQEGKARKTNPFIQSTLRKRLYLQ 96
DB 207 TEVTRMAEALVQEGKARKTNPFIQSTLRKRLYLQ 242

RESULT 2
ICB3 MOUSE STANDARD; PRT; 257 AA.
AC 089094;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-14 precursor (EC 3.4.22.-) (CASP-14) (MICE).
GN CASP14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=C57BL/6J;
RX MEDLINE=99040667; PubMed=9823333;
RA Ahmed M., Srinivasula S.M., Hegde R., Mukattash R.,
RA Fernandes-Alnemri T., Alnemri E.S.;
RT "Identification and characterization of murine caspase-14, a new
member of the caspase family.";
RL Cancer Res. 58:5201-5205(1998).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J TISSUE=Embryo;
RX MEDLINE=99222069; PubMed=10203698;
RA Van de Craen M., Van Looy G., Pype S., Van Criekinge W.,
RA Van den Brande I., Molemans F., Fiers W., Declercq W.,
RA Vandenbeke P.;
RT "Identification of a new caspase homologue: caspase-14.";
RL Cell Death Differ. 5:838-846(1998).
RN 13
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-136.
RX MEDLINE=99009076; PubMed=9792675;
RA Hu S., Snipas S.J., Vincenz C., Salvesen G., Dixit V.M.;
RT "Caspase-14 is a novel developmentally regulated protease.";
RL J. Biol. Chem. 273:29648-29653(1998).
CC -1- FUNCTION: Seems to be involved in the death receptor and granzyme
transducer of cell death. May play a role in ontogenesis and skin
physiology.
CC -1- SUBUNIT: May dimerize with large prodomain caspases.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
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CC -1- TISSUE SPECIFICITY: Embryo, adult liver and less in adult brain
and kidney.
CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-8 AND -10 GENERATES THE
TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
PROPEASE.
CC -1- SIMILARITY: Belongs to peptidase family C14.
-----
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or send an email to license@isb-sib.ch).
-----
DR EMBL: AF092997; AAC63364.1; -.
DR EMBL: AJ007750; CAA07678.1; -.
DR HSSP: P29466; 1ICE.
DR MEROPS: C14.018; -.
DR MGD: MGI:1335092; Casp14.
DR GO: GO:0006917; P:induction of apoptosis; IDA.
DR InterPro: IPR002138; ICE p10.
DR InterPro: IPR001309; ICE p20.
DR InterPro: IPR002398; Peptidase C14.
DR Pfam: PF00656; Peptidase C14; 1.
DR PRINTS: PR00376; ILICENZTME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01121; CASPASE_HIS; FALSE_NEG.
DR PROSITE: PS01122; CASPASE_CYS; FALSE_NEG.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KM HydroLase; Thiol protease; Apoptosis; Zymogen.
FT PROPP 1 7
FT CHAIN 1 8 CASPASE-14 SUBUNIT P18 (POTENTIAL).
FT CHAIN 2 257 CASPASE-14 SUBUNIT P11 (POTENTIAL).
FT ACT SITE 93 93 BY SIMILARITY.
FT ACT SITE 136 136 BY SIMILARITY.
FT ACT SITE 136 136 C->A: DECREASE IN DEATH-INDUCING
ACTIVITY.
FT MUTAGEN 136 136
SQ SEQUENCE 257 AA; 29458 MW; A228D88DFBA0EB84 CRC64;

Query Match 73.3%; Score 357; DB 1; Length 257;
Best Local Similarity 70.2%; Pred. No. 2.1e-30;
Matches 66; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 3 VVWVXKDSPTPTPTDHALHVSTVEGYIAYRHDKGSCFIQTLDVFTKRKGIIEILLTE 62
DB 164 VVWVXKDSPTPTPTDHALHVSTVEGYIAYRHDKGSCFIQTLDVFTKRKGIIEILLTE 223
QY 63 VTRMAEALVQEGKARKTNPFIQSTLRKRLYLQ 96
DB 224 VTRMAEALVQEGKARKTNPFIQSTLRKRLYLQ 257

RESULT 3
ICB3 MOUSE STANDARD; PRT; 277 AA.
AC P70677; O08668; Q90W14;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (cysteine protease CPP32) (Yama
protein) (CPP-32) (Caspase-3) (SREB cleavage activity 1)
DE (SCA-1) (LICE).
GN CASP3 OR CPP32.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
```

RA Juan T.S.-C., McNamee I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling interleukin-1 beta converting enzyme
RT and CED-3.";
RL Oncogene 13:749-755 (1996) .
RN [21]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224429; PubMed=9070089;
RA Nakase T., Uraae K., Momoi M.Y., Kimura I., Momoi T.;
RT "Specific expression of CPP32 in sensory neurons of mouse embryos and
RT activation of CPP32 in the apoptosis induced by a withdrawal of
RT NGF.";
RL Biochem. Biophys. Res. Commun. 231:770-774 (1997) .
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX van de Craen M., Vandenaabeele P., Declercq W., van den Brande I.,
RA van Leo G., Molemans F., Schotte P., van Criekinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69 (1997) .
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [51]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N. TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Staussner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditchenko L., Marinska K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares B., Bonaldi M.F., Casavari T.L., Schetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Garincci P., Prange C.,
RA Raza S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzanski M.I., Skalka U., Smalls D.E.,
RA Schermer A., Schein J.B., Jones S.U.M., Marra W.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002) .
RN [61]
RP SEQUENCE OF 58-277 FROM N.A.
RA Denis F., Alam A., Cohen L., Hartgers F., Braun M., Martinez O.,
RA Fortin J.-P., Sekaly R.-P.;
RT "Multiple pathways of apoptosis converging on the CPP32 protease.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [1]
RP FUNCTION: Involved in the activation cascade of caspases
RP responsible for apoptosis execution. At the onset of apoptosis it
RP proteolytically cleaves poly(Adp-ribose) polymerase (PAR) at a
RP 216-Asp1-Gly-217 bond. Cleaves and activates steroid regulatory
RP element binding proteins (SRBPs) between the basic helix-loop-
RP helix leucine zipper domain and the membrane attachment domain.
RP Cleaves and activates caspase-6, -7 and -9 (By similarity).
RP Cleaves IL-1 beta between an Asp and an Ala, releasing the mature
RP cytokine which is involved in a variety of inflammatory processes
RP [By similarity].
RP SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
RP (By similarity).
RN [1]
RP SUBCELLULAR LOCATION: Cytoplasmic.
RN [1]
RP TISSUE SPECIFICITY: Highest expression in spleen, lung, liver,
RP kidney and heart. Lower expression in brain, skeletal muscle and
RP testis.

```

-1- PMW CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROPEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7, PROPEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U54803; AAC52768.1; -.
DR EMBL; U54802; AAC52768.1; JOINED.
DR EMBL; U49929; AAC52764.1; -.
DR EMBL; D86352; BAA21727.1; -.
DR EMBL; Y13086; CAA73528.1; -.
DR EMBL; U19522; AAC53196.1; -.
DR EMBL; BC038825; AAH8825.2; -.
DR EMBL; U63720; AAD09504.1; -.
DR PTR; JC5410; JC5410.
DR HSSP; P42574; IPRX0.
DR MEROPS; C14.003; -.
DR MGD; MGI:107739; Caep3.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; I.
DR PRINTS; PRO0376; ILIBCNZYME.
DR SMART; SMO0115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_F20; 1.
KW Hydrolase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT CHAIN 10 28
FT CHAIN 29 175
FT CHAIN 176 277
FT ACT_SITE 121 121
FT ACT_SITE 163 163
FT CONFLICT 17 17
FT CONFLICT 51 51
FT CONFLICT 63 65
FT CONFLICT 84 84
FT CONFLICT 95 95
FT CONFLICT 97 97
FT CONFLICT 128 128
FT CONFLICT 135 135
FT CONFLICT 231 231
FT CONFLICT 262 262
SQ SEQUENCE 277 AA; 31474 MW; CE91598FV482605 CRC64;
Query Match 25.3%; Score 123; DB 1; Length 277;
Best Local Similarity 39.6%; Pred.No.1.le-05;
Matches 36; Conservative 11; Mismatches 36; Indels 8; Gaps 3
QY 11 QTIPTYTDAHVYSTVGEYIAYVRHDQKSCPTQTVLVDFYRKGHILE--LITVTRRM 67
DB 185 QKIPVEADFLVAVYSTAPGYSSWRNKGDSWFIQSLCSML-KLYAHKLEFMMILTVNRKV 243
QY 68 A-----EALVQEGKARKNTNPQLQSTLRKRLY 94
DB 244 ATEPESFSLDSTFHAKQIPICVSMLTRELY 274

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AC P42573; P45435; Q9GQ4; Q9NA08;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cell death protein 3 precursor (EC 3.4.22.-).
 GN CED-3 OR C48D1.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peleodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A. AND MUTAGENESIS.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94061982; PubMed=8242740;
 RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
 RT "The C. elegans cell death gene ced-3 encodes a protein similar to
 RL Cell 75:641-652(1993)."
 RN [2]
 RP REVISION TO 418.
 RA Horvitz H.R.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Burton J.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -! FUNCTION: Acts as a cysteine protease in controlling programmed
 CC cell death by proteolytically activating or inactivating a
 CC substrate protein or proteins, a potential substrate may be ced-4.
 CC Alternatively it might directly cause cell death by
 CC proteolytically cleaving proteins that are crucial for cell
 CC viability.
 CC -! SUBUNIT: Could be a heterodimer of two subunits derived from the
 CC precursor sequence by a probable autocatalytic mechanism.
 CC -! DEVELOPMENTAL STAGE: Most abundant during embryogenesis and is
 CC also detected at later stages.
 CC -! PTM: May be regulated by phosphorylation.
 CC -! SIMILARITY: Belongs to peptidase family C14.
 CC -! SIMILARITY: Contains 1 CARD domain.
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 CC -----
 DR EMBL; L29052; AAA72982.2; -;
 DR EMBL; AF210702; AAG42045.1; -;
 DR EMBL; Z81049; CAB61001.2; -;
 DR PIR; A49429; A49429.
 DR HSSP; P42574; 1CP3.
 DR MOROPS; C14.002; -;
 DR WormPep; C48D1.2; CE29088.
 DR InterPro; IPR001315; CARD.
 DR InterPro; IPR002138; ICE_p10.
 DR InterPro; IPR001309; ICE_p20.
 DR InterPro; IPR002398; Peptidase_C14.
 DR Pfam; PF00619; CARD; 1.
 DR Pfam; PF00656; Peptidase_C14; 1.
 DR PRINTS; PR00376; ILIBENZYME.
 DR SMART; SM00114; CARD; 1.
 DR SMART; SM00115; CASC; 1.
 DR PROSITE; PS02009; CARD; 1.
 DR PROSITE; PS01122; CASPASE_CYS; 1.
 DR PROSITE; PS01121; CASPASE_HIS; 1.
 DR PROSITE; PS0207; CASPASE_P10; 1.

DR PROSITE; PS02008; CASPASE_P20; 1.
 KW Hydrolase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.
 FT CHAIN 1 371
 FT
 FT CHAIN 372 503
 FT
 FT DOMAIN 1 91
 FT DOMAIN 107 205
 FT ACT_SITE 304 304
 FT ACT_SITE 358 358
 FT MOTAGEN 27 27
 FT MOTAGEN 65 65
 FT MOTAGEN 360 360
 FT MOTAGEN 449 449
 FT MOTAGEN 466 466
 FT MOTAGEN 483 483
 FT MOTAGEN 486 486
 FT MOTAGEN 486 486
 SQ SEQUENCE 503 AA; 56616 MW; 722D5831F94DAA69 CRC64;
 Query Match 25.2%; Score 122.5; DB 1; Length 503;
 Best Local Similarity 34.5%; Pred. No. 2.4e-05;
 Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;
 QY 14 PVTYDALHYVSTVEGYIAYRHQKSCFIQTLDVFT--KRGHILELTVRRNAEAE 71
 Db 410 PSQADILIVATYAQVSWRNRSARGSWFIQAVCEVSTHAKMDVVELLTVAKKVAACGF 469
 QY 72 LVDEG-KARKNPEIQSTLRKLY 94
 Db 470 QTSQSGNIUKOMPEMSTRLLKKEY 493
 RESULT 5
 ICES_CRILO STANDARD; PRT; 277 AA.
 AC Q60431;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
 DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
 DE (SCA-1).
 GN CASP3 OR CPP32.
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96183185; PubMed=8605870;
 RA Wang X., Zelenksi N.G., Yang J., Sakai J., Brown M.S.,
 RA Goldstein J.L.;
 RT "Cleavage of sterol regulatory element binding proteins (SREBPs) by
 RT CPP32 during apoptosis".
 RL EMBO J. 15:1012-1020(1996).
 CC -! FUNCTION: Involved in the activation cascade of caspases
 CC responsible for apoptosis execution. At the onset of apoptosis it
 CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
 CC 216-Asp-1-Gly-217 bond. Cleaves and activates sterol regulatory
 CC element binding proteins (SREBPs) between the basic helix-loop-
 CC helix leucine zipper domain and the membrane attachment domain.
 CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
 CC -! SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
 CC (By similarity).
 CC -! SUBCELLULAR LOCATION: Cytoplasmic.
 CC -! PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
 CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
 CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
 CC PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
 CC CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
 CC VICE VERSA (BY SIMILARITY).

CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U27463; AAB01511.1; -
DR HSSP: P42574; 1PAU.
DR MEROPS: C14.003; -
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILBCEZYME.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.
KM Hydrolyase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.
FT CHAIN 176 277 APOPAIN P12 SUBUNIT.
FT ACT SITE 121 121 BY SIMILARITY.
FT ACT SITE 163 163 BY SIMILARITY.
SQ SEQUENCE 277 AA; 31612 MW; 0BF8A4590A2828A3 CRC64;

Query Match 25.1%; Score 122; DB 1; Length 277;
Best Local Similarity 39.6%; Pred. No. 1.4e-05;
Matches 36; Conservative 11; Mismatches 36; Indels 8; Gaps 3;

QY 11 CQIPPTDAHYSTVEGYIAVRHDKSGCFTQTDVFTYKRGHLE---LITETARM 67
DB 185 QKTPVADFLVATSPGYSWKPNQSGWFIQSLCSM-KYAHKLEPHITRVNRY 243
QY 68 A---EALVQEGKAKTNPEIQSTLRKLY 94
DB 244 ATEFESFSLDSTPHAKQIPCIYSMLTKELY 274

RESULT 6
ID ICE3 RAT STANDARD; PRT; 277 AA.
AC P55213; P70543; P97699; Q62993;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1) (ILCE) (IRP).
GN CASP3 OR CPP32.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96358624; PubMed=8761296;
RA Juan T.S.-C., McNeice I.K., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Fletcher F.A.;
RT "Molecular characterization of mouse and rat CPP32 beta gene encoding
RT a cysteine protease resembling interleukin-1 beta converting enzyme
RT and CED-3.";
RL Oncogene 13:749-755 (1996).
RN [2]
RP SEQUENCE OF 30-241 FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96042508; PubMed=7588240;

RA Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I.,
RA Hirschfield A.N., Tilly J.L.;
RT "Interleukin-1 beta-converting enzyme-related proteases (IRPs) and
RT mammalian cell death: dissociation of IRP-induced oligonucleosomal
RT endonuclease activity from morphological apoptosis in granulosa cells
RT of the ovarian follicle.";
RL Endocrinology 136:5042-5053 (1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97184204; PubMed=9030616;
RA Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
RA Rostock P. Jr., Poirier G.G., Paul S.M.;
RT "Cloning and expression of a rat brain interleukin-1beta-converting
RT enzyme (ICE)-related protease (IRP) and its possible role in
RT apoptosis of cultured cerebellar granule neurons.";
RL J. Neurosci. 17:1561-1569 (1997).
RN [4]
RP SEQUENCE OF 1-264 FROM N.A.
RA Yakovlev A.G.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. At the onset of apoptosis it
CC proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a
CC 216-Asp-Gly-217 bond. Cleaves and activates sterol regulatory
CC element binding proteins (SREBPs) between the basic helix-loop-
CC helix leucine zipper domain and the membrane attachment domain.
CC Cleaves and activates caspase-6, -7 and -9 (By similarity).
CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12) subunit
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE
CC BUT NOT IN KIDNEY OR TESTIS.
CC -1- DEVELOPMENTAL STAGE: Highly expressed in neuron-enriched regions
CC of the developing brain, but down-regulated to low levels in the
CC adult brain.
CC -1- PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES THE
CC TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS
CC LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED
CC PROPEASE-7. PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AND
CC VICE VERSA (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U49930; AAC52765.1; -
DR EMBL: U34685; AAC52261.1; -
DR EMBL: U84410; AAC41792.1; -
DR EMBL: U58656; AAB02722.1; -
DR PIR: I67437; I67437.
DR HSSP: P42574; 1PAU.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILBCEZYME.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.
KM Hydrolyase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 9
FT PROPEP 10 28 BY SIMILARITY.
FT CHAIN 29 175 APOPAIN P17 SUBUNIT.

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FT CHAIN 176 277 APOFAPIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT CONFLICT 25 29 KSMDS -> QVD (IN REF. 4).
FT CONFLICT 170 170 C -> S (IN REF. 2).
FT CONFLICT 178 178 T -> A (IN REF. 2).
FT CONFLICT 182 182 M -> V (IN REF. 2).
FT CONFLICT 187 187 I -> K (IN REF. 2).
FT CONFLICT 190 190 E -> G (IN REF. 3).
FT CONFLICT 199 199 T -> S (IN REF. 2).
FT CONFLICT 211 211 D -> G (IN REF. 2).
FT CONFLICT 236 236 T -> I (IN REF. 4).
FT CONFLICT 245 245 T -> M (IN REF. 3).
SQ SEQUENCE 277 AA; 31491 MW; ADABF418E2507402 CRC64;

Query Match 24.6%; Score 120; DB 1; Length 277;
Best Local Similarity 39.6%; Pred. No. 2.2e-05;
Matches 36; Conservative 10; Mismatches 37; Indels 8; Gaps 3;

QY 11 QITPTDALHYVSTVEGYIAYRHDKSGCFIOTLVFTFKRGHIDE--LTLEVTFRM 67
DB 185 QKIPVEADFLYASTAGYYSWNRSGSWFIQSLC-AMLKIVAHKLEFPHIILTRVRKY 243
QY 68 A---EAEIVQEGKARKTNPFIQSTLRKRLY 94
DB 244 ATEFESEFLDTEFAKKQIPCIIVSMILTKELY 274

RESULT 7
CEB3_CAEVU STANDARD; PRT; 496 AA.
ID CEB3_CAEVU STANDARD; PRT; 496 AA.
AC P45436;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell death protein 3 precursor (EC 3.4.22.-).
GN CED-3.
OS Caenorhabditis vulgaris.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=31233;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94061982; PubMed=8242740;
RA Yuan J., Shaham S., Ledoux S., Ellis H.M., Horvitz H.R.;
RT "The C. elegans cell death gene ced-3 encodes a protein similar to
RT mammalian interleukin-1 beta-converting enzyme."
RL Cell 75:641-652(1993).
CC -1- FUNCTION: Acts as a cysteine protease in controlling programmed
CC cell death by proteolytically activating or inactivating a
CC substrate protein or proteins, a potential substrate may be ced-4.
CC Alternatively it might directly cause cell death by
CC proteolytically cleaving proteins that are crucial for cell
CC viability (By similarity).
CC -1- SUBUNIT: Could be a heterodimer of two subunits derived from the
CC precursor sequence by a probable autocatalytic mechanism.
CC -1- PTM: May be regulated by phosphorylation.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
DR HSSP: P42574; ICP3.
DR MEROPS: C14.002; -.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILIBENZYME.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00115; CASG; 1.
DR PROSITE: PS50209; CARD; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.

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DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
DR Hydrolyase; Thiol protease; Zymogen; Apoptosis; Phosphorylation.
FT CHAIN 1 364 CELL DEATH PROTEIN 3 SUBUNIT 1
FT CHAIN 365 496 (POTENTIAL).
FT CHAIN 365 496 CELL DEATH PROTEIN 3 SUBUNIT 2
FT DOMAIN 1 91 (POTENTIAL).
FT ACT_SITE 308 308 CARD.
FT ACT_SITE 351 351 BY SIMILARITY.
SQ SEQUENCE 496 AA; 55945 MW; 58E73C790DC3BD38 CRC64;

Query Match 24.5%; Score 119.5; DB 1; Length 496;
Best Local Similarity 34.5%; Pred. No. 4.8e-05;
Matches 29; Conservative 19; Mismatches 33; Indels 3; Gaps 2;

QY 14 PTYTDAHYVSTVEGYIAYRHDKSGCFIOTLVFT--RKGHILELTVTRRNAAE 71
DB 401 PSQADILIRYATTAQYVSWNRSGSWFIQAVCEVSTHAKMDVVELLTVNKKVACGF 460
QY 72 LVQEG-KARKTNPFIQSTLRKRLY 94
DB 461 QTSQGANITIKQMPMTSRLTKFY 484

RESULT 8
ICE7_MOUSE STANDARD; PRT; 303 AA.
ID ICE7_MOUSE STANDARD; PRT; 303 AA.
AC P97864; 008669;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE2 cysteine protease) (Apoptotic
DE protease Mch-3).
GN CASP7 OR MCH3 OR LICE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RA Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
RT CP32 beta, interleukin-1 beta converting enzyme, and CED-3."
RL Genomics 40:86-93(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236307; PubMed=9125129;
RA Mukasa T., Khoroku Y., Tsukahara T., Momoi M.Y., Kimura I.,
RA Momoi T.;
RT "Wormannin enhances CP32-like activity during neuronal
RT differentiation of P19 embryonal carcinoma cells induced by retinoic
RT acid."
RL Biochem. Biophys. Res. Commun. 232:192-197(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaebelle P., Declercq W., van den Brande I.,
RA van Ioo G., Molemans F., Schotte P., van Crickinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members."
RL FEBS Lett. 403:61-69(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maita M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves and activates steryl
CC regulatory element binding proteins (SREBPs). Overexpression
CC promotes programmed cell death (By similarity).
CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND
CC KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
CC EXPRESSION IN THE BRAIN.
CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.

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CC or send an email to license@sb-sib.ch).

DR EMBL: U67321; AAC53068.1; ALT_INIT.
DR EMBL: D86353; BAA19730.1; -.
DR EMBL: Y13086; CAAY3530.1; -.
DR EMBL: BC005428; AAH05428.1; -.
DR HSSP: P42574; IPAU.
DR MEROB: C14.004; -.
DR MGD: MGI:109383; Casp7.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; IL1BCENZME.
DR SMART: SM00115; CASC; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydroxylase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20 (BY SIMILARITY).
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303
FT ACT SITE 144 144 CASPASE-7 SUBUNIT P11 (BY SIMILARITY).
FT ACT SITE 186 186 BY SIMILARITY.
FT CONFLICT 10 11 EL -> DW (IN REF. 2).
FT CONFLICT 45 45 A -> T (IN REF. 2).
FT CONFLICT 48 49 VR -> RQ (IN REF. 2).
SQ SEQUENCE 303 AA; 34060 MW; 7477878B5BDE5F744 CRC64;

Query Match 23.4%; Score 114; DB 1; Length 303;
Best Local Similarity 36.4%; Pred. No. 0.00011;
Matches 32; Conservative 12; Mismatches 38; Indels 6; Gaps 2;

OY 13 IPTYDALHYSTVSGYLAHYRHDQKSGCFIOTLVDFPK--RKGHILELFEVTRMAEA 70
DB 213 IPVEDPFLFASTVGVGYSMRNPQSGMFWQALCSILNEHKGDLFIQTLIVNDRVARR 272
OY 71 ELVQEGKAR---KTNPETIOSTLRKRLY 94
DB 273 FESQSDPDRFNKKQIPCMVSNLTRELY 300
RESULT 9
ID ICE3 HUMAN STANDARD; PRT; 277 AA.
AC P42574; Q96AN1; Q96KX2;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama
DE protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
DE (SCA-1).
GN CASP3 OR CPP32.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RC TISSUE=T-cell;
RX MEDLINE=95074098; PubMed=7983002;
RA Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
RT "CPP32, a novel human apoptotic protein with homology to
RT Caenorhabditis elegans cell death protein Ced-3 and mammalian
RT interleukin-1 beta-converting enzyme.";
RL J. Biol. Chem. 269:30761-30764(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95292347; PubMed=7774019;
RA Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
RA Beidler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;
RT "Yama/CPP32 beta, a mammalian homologue of CED-3, is a CrmA-inhibitable
RT protease that cleaves the death substrate poly(ADP-ribose)
RT polymerase.";
RL Cell 81:801-809(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Vallette F.M., Oliver J.J.;
RT "Control of the activation of the procaspase-3 by a sequence located
RT at the N-terminus of the p17 subunit.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT GLU-190.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

CC -1- TISSUE SPECIFICITY: Highly expressed in lung, spleen, heart, liver
CC and kidney. Moderate levels in brain and skeletal muscle, and low
CC in testis. Also found in many cell lines, highest expression in
CC cells of the immune system.
CC -1- P1M: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
CC GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE
CC PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE
CC ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
CC OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
CC AND VICE VERSA.
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U13737; AAA65015.1; -;
DR EMBL; U13738; AAB60355.1; -;
DR EMBL; U26943; AAA74929.1; -;
DR EMBL; AJ413265; CAC88866.1; -;
DR EMBL; AY219866; AAO25654.1; -;
DR EMBL; BC016926; AAH16926.1; -;
DR PIR; A55315; A55315.
DR PDB; 1PAU; 07-JUL-97.
DR PDB; 1CP3; 24-DEC-97.
DR PDB; 1GFW; 23-JUN-00.
DR MEROPS; C14.003; -;
DR Genew; HGNC:1504; CASP3.
DR MIM; 600636; -;
DR GO; GO:0004208; F:caspase-3 activity; TAS.
DR GO; GO:0008624; P:induction of apoptosis by extracellular sig. .; TAS.
DR GO; GO:0008629; P:induction of apoptosis by intracellular sig. .; TAS.
DR GO; GO:0009405; P:pathogenesis; TAS.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00655; Peptidase_C14; 1.
DR PRINTS; PR00376; TLICBENZME.
DR SMART; SM00115; CASC; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydroxylase, Thiol protease, Zymogen, Apoptosis, Polymorphism;
KW 3d-structure.
KW PROPEP 1 9
FT PROPEP 10 28
FT CHAIN 29 175 APOBAIN P17 SUBUNIT.
FT CHAIN 176 277 APOBAIN P12 SUBUNIT.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT VARIANT 190 190 D->E (in isoform beta).
FT CONFLICT 31 36 /FTId=VAR_001401.
FT STRAND 36 36 ISLDS -> MSWDTG (IN REF. 3).
FT STRAND 43 51
FT HELIX 57 59
FT TURN 60 60
FT TURN 65 66
FT HELIX 67 80
FT TURN 81 82

Query Match 22.4%; Score 109; DB 1; Length 277;
Best Local Similarity 37.5%; Pred. No. 0.0003;
Matches 33; Conservative 13; Mismatches 36; Indels 6; Gaps 3;

13 IPVTDAIAVSYVEGYIAVRHQQSGCFIQTIVDFETK--RKSHILELLETVRRMA-E 69
187 IPVDADLVAVSYAVDPGYVSWRNSNDGSGWFIOSICAMKQVADKIFEMHITITRVNPKVATTE 246

QY 70 ABLVQ---EGKARKTNPEIQSTLRKRLY 94
DB 247 FESFSDATFHAKQIPICIVSMILTKELY 274

RESULT 10
ICE3_XENLA STANDARD; PRT; 282 AA.
AC P55866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Apoptain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Caspase-3)
GN CASP3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184166; PubMed=9030578;
RA Yaoita Y., Nakajima K.;
RT "Induction of apoptosis and CPP32 expression by thyroid hormone in a
myoblastic cell line derived from tadpole tail";
RL J. Biol. Chem. 272:5122-5127(1997).
CC -1- FUNCTION: Important mediator of apoptosis. At the onset of
apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase
(PARP) at a 216-Asp-Gly-217 bond (By similarity).
CC -1- SUBUNIT: Heterodimer of a 17 kDa (p17) and a 12 kDa (p12)
subunits.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- MISCELLANEOUS: The subunits are derived from the precursor
sequence by a probable autocatalytic mechanism and probably by
other caspases (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL: D89784; BAA14018.1; -
DR HSSP: P42574; 1PNU.
DR MEROPS: C14.003; -
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase C14.
DR Pfam: PF00656; Peptidase C14; 1.
DR PRINTS: PR00376; TLBCENZYM.
DR SMART: SM00115; CASG; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS0207; CASPASE_P10; 1.
DR PROSITE: PS0208; CASPASE_P20; 1.
KW Hydroxylase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 ?
FT CHAIN ? 186
FT ACT SITE 187 282
FT ACT SITE 131 131
FT ACT SITE 174 174
SQ SEQUENCE 282 AA; 32124 MW; CB390E8980CAB77F CRC64;
Query Match 22.0%; Score 107; DB 1; Length 282;
Best Local Similarity 34.1%; Pred. No. 0.00053;
Matches 31; Conservative 15; Mismatches 39; Indels 6; Gaps 3;
QY 7 KSPQTIPIFYDALMIVSYVSGYIAVRHQKSCFIQTLVDVFTKRKH-ILLELTFTV 64

DB 192 REEIRIPVEADFLTAIVSTVPGYCSWRDMOSWPIQSLCKMIKLYGSHLELIQILTCVN 251
QY 65 RRMV-EAEIVQEGKARKTNPEIQSTLRKRLY 94
DB 252 HMVADLPFTFH---AKQIPCVVSMILTKSFY 279

RESULT 11
ICE7_HUMAN STANDARD; PRT; 303 AA.
AC P55210; Q13364; Q96B80;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
GN CASP7 OR MCH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=96139498; PubMed=8576161;
RA Duan H., Chinnaiyan A.M., Hudson P.L., Wing J.P., He W.-W.,
RT Dixit V.M.;
RL "ICE-LAP3, a novel mammalian homologue of the Caenorhabditis elegans
cell death protein Ced-3 is activated during Fas- and tumor necrosis
factor-induced apoptosis";
RL J. Biol. Chem. 271:1621-1625(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Spleen;
RX MEDLINE=96147144; PubMed=8567622;
RA Lipke J.A., Gu Y., Sarnecki C., Caron P.R., Su M.S.-S.;
RT "Identification and characterization of CPP32/Wch2 homolog 1, a novel
cysteine protease similar to CPP32";
RL J. Biol. Chem. 271:1825-1828(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=T-cell;
RX MEDLINE=96105019; PubMed=8521391;
RA Fernandes-Alnemri T., Takahashi A., Armstrong R.C., Krebs J.,
RA Fritsch L.C., Tomasek J.J., Wang L., Yu Z., Croce C.M., Salveson G.,
RT Farshaw W.C., Litwack G., Alnemri E.S.;
RT "Mch3, a novel human apoptotic cysteine protease highly related to
CPP32";
RL Cancer Res. 55:6045-6052(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND ALPHA').
RC TISSUE=fetal lung, and Fetal spleen;
RX MEDLINE=97224489; PubMed=9070923;
RA Juan T.S.-C., McInnes I.K., Argento J.M., Jenkins N.A., Gilbert D.J.,
RT Copeland N.G., Fletcher F.A.;
RT "Identification and mapping of Casp7, a cysteine protease resembling
CPP32 beta, interleukin-1 beta converting enzyme, and CED-3";
RL Genomics 40:86-93(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Wang S.U.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Millange S.U.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunnatne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.D., Lu X., Gibbs R.A.,

DR	GO;	GO:0008234;	Cysteine-type peptidase activity; TAS.
DR	GO;	GO:0008632;	Papoptotic program; TAS.
DR	InterPro;	IPR002138;	ICE p10.
DR	InterPro;	IPR001309;	ICE p20.
DR	InterPro;	IPR002398;	Peptidase Cl4.
DR	pfam;	PF00656;	Peptidase Cl4; I.
DR	PRINTS;	PRO0376;	TILBENZYM.
DR	SMART;	SMO0115;	Casp; 1.
DR	PROSITE;	PS01122;	CASPASE_CYS; 1.
DR	PROSITE;	PS01121;	CASPASE_HIS; 1.
DR	PROSITE;	PS50207;	CASPASE_P10; 1.
DR	PROSITE;	PS50208;	CASPASE_P20; 1.
KW	Hydrolase,	hydrol protease;	Zymogen; Apoptosis; Alternative splicing;
KW	3D-structure.		
FT	PROPEP	1	23
FT	CHAIN	24	198
FT	PROPEP	199	206
FT	CHAIN	207	303
FT	ACT_SITE	144	144
FT	ACT_SITE	186	186
FT	VARSPLIC	1	1
FT			M -> MDCVMPGPKWHLEKNNSCGSGSICASYTQM (in isoform Alpha'). /FtId-VSP_000806
FT	VARSPLIC	149	303
FT			VTKGDVTVTFIKDTLTHAFNRDRCKTLLEKPLFIQACRGTELDGIDGADSGPINDDANRYKIPEADFLEFASTVPGYXSWRPGRGSWFVQALCSILEHSGMDLEIMQILTRVNDVRARHFESOSDPPHFHEKKQIPEVSHMLTELKELYSQ -> MESCSVTGGVORRLDGLRIQPPPELAGSLMMSRPGRGSMOMLIIDTPRSQMKLTSSSIPIPRFOALTIRGAGDEAPACKPSPA PMSRTERTKMTKSCRSSPG (in isoform Beta). /FtId=VSP_000807. C->A: NO APOPTOTIC ACTIVITY. D -> E (IN REF. 5). G -> A (IN REF. 1).
FT	MUTAGEN	186	186
FT	CONFLICT	4	4
FT	CONFLICT	194	194
SO	SEQUENCE	303 AA;	34276 MW; CD373EBS4A232C4 CRC64;
	Query Match		22.0%; Score 107; DB 1; Length 303; Best Local Similarity 34.1%; Pred. No. 0.00058;
	Matches 30;	Conservative 13;	Mismatches 39; Indels 6; Gaps 2;
Oy	13	IPTYDALHYSTVEGIATRHQKSGCFIQTLVDVTK--RKGHILELTETRRMAEA	70
Db	213	IPVADFLFAFYASTYPPGYVSRWSRSGSWFQALCSILEHSGMDLEIMQILITRVNDRVARH	272
Oy	71	ELVSEG---KARKNPDIOSTLRKLRY	94
Db	273	FESOSDDPHFEKKQIPECVVSMTELKELY	300

RESULT 12

ICE7_MESAU STANDARD; PRY; 303 AA.

AC PSE214; 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, last sequence update)

DT 28-FEB-2003 (Rel. 41, last annotation update)

DE Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 3)
(ICE-IAP3) (Apoptotic protease Mch-3) (SRBP cleavage activity 2)
(SCA-2).

DN CASP7 OR MCH3.

OS Mesocricetus auratus (Golden hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
CC Mesocricetus

CC NCBI_Taxid=10036;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=Syrian; TISSUE=Liver;

RX MEDLINE=96224303; Pubmed=8643593;

RA Pai J.-T., Brown M.S., Goldstein J.L.;
"Purification and cDNA cloning of a second apoptosis-related cysteine
protease that cleaves and activates steroid regulatory element binding
proteins.";

CC Proc. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves and activates sterol
CC regulatory element binding proteins (SREBPs). Proteolytically
CC cleaves poly(ADP-ribose) polymerase (PARP) at a 216-Asp-Gly-217
CC bond. Overexpression promotes programmed cell death (by
CC similarity).
CC -1- SUBUNIT: Heterodimer of a 20 kDa (p20) and a 11 kDa (p11) subunit
CC (by similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE
CC SUBUNITS. PROPEPTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
CC CPB2 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF
CC CASPASE-7 AND THE LARGE SUBUNIT OF CPB2 PROTEASE ALSO OCCUR AND
CC VICE VERSA (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC -----
DR EMBL; U47332; AAC52595.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.004; -.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Zymogen; Apoptosis.
FT PROPEP 1 23
FT CHAIN 24 198 CASPASE-7 SUBUNIT P20.
FT PROPEP 199 206 BY SIMILARITY.
FT CHAIN 207 303 CASPASE-7 SUBUNIT P11.
FT ACT SITE 144 144 BY SIMILARITY.
FT ACT SITE 186 186 BY SIMILARITY.
SQ SEQUENCE 303 AA; 34037 MW; EA23356D90984648 CRC64;
Query Match 22.0%; Score 107; DB 1; Length 303;
Best Local Similarity 35.2%; Pred. No. 0.00058;
Matches 31; Conservative 15; Mismatches 36; Indels 6; Gaps 3;
QY 13 IPYVTAALHYSTVEGYIAYRHQKSGCFIQTVDVFTK--RKGHILELTETWRMA-- 68
Db 213 IPEADPELFAYSTVPGYVSRNPKGSWFQALCSILDEHKKOLEIMQILTRNDVARR 272
QY 69 -EALVQE-GKARTNPEIOSITLRKLY 94
Db 273 FESQCDPCEPKKQIJCWVSMITKELY 300
RESULT 13
ICED_CHICK
ID ICE2_CHICK STANDARD; PRT; 424 AA.
AC Q98943;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (ICH-
DE 11/15).
GN CASP2 OR ICH1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

CC Gallus.
CC NCBI_TaxID=9031;
CC [1]
CC SEQUENCE FROM N.A. (ISOFORMS ICH-1L AND ICH-1S).
CC STRAIN=White Leghorn; TISSUE=Ovarian granulosa.
CC MEDLINE=97368127; PubMed=9224894;
CC Johnson A.L., Bridgman J.T., Bergeron L., Yuan J.;
CC "Characterization of the avian ICH-1 cDNA and expression of ICH-1L
CC mRNA in the hen ovary.";
CC RNA 192:227-233 (1997).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival (by similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=ICH-1L;
CC IsoId=Q98943-1; Sequence=Displayed;
CC Note=Only form found in the ovary;
CC Name=ICH-1S;
CC IsoId=Q98943-2; Sequence=VSP_000803, VSP_000804;
CC Gene 192:227-233 (1997).
CC -1- PTM: Heterodimer of a small and a large subunit (by similarity).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
CC -----
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CC -----
DR EMBL; U64963; AAC29881.1; ALU_INIT.
DR HSSP; P42574; 1CP3.
DR MEROPS; C14.006; -.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE p10.
DR InterPro; IPR001309; ICE p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCNZYME.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
FT PROPEP 1 140
FT CHAIN 141 308 CASPASE-2 SUBUNIT P18 (BY SIMILARITY).
FT CHAIN 309 424 CASPASE-2 SUBUNIT P13 (BY SIMILARITY).
FT CHAIN 315 424 CASPASE-2 SUBUNIT P12 (BY SIMILARITY).
FT DOMAIN 7 96 CARD.
FT ACT SITE 248 248 BY SIMILARITY.
FT ACT SITE 291 291 BY SIMILARITY.
FT VARSPLIC 1 7 Missing (in isoform ICH-1S).
FT VARSPLIC 294 424 /FTId=VSP_000803.
FT VARSPLIC 294 424 /FTId=VSP_000804.
SQ SEQUENCE 424 AA; 47959 MW; 79281050838B2F60 CRC64;
Query Match 21.5%; Score 104.5; DB 1; Length 424;
Best Local Similarity 31.5%; Pred. No. 0.0015;
Matches 29; Conservative 21; Mismatches 29; Indels 13; Gaps 3;

```

QY 13 IPTYDALHVSVEGYIAVRHDKGSCFTQTVDFYTK--RKGHILELTYTRMAEA 70
DB 329 LPTPSDMICGACLKGMNAAMRNTRGSGWYIEALTTFVAEDSRDTHVADMVKNVRLKQ- 387
QY 71 ELVDEGKARKTN-----PEIOSTLRRLYL 95
DB 388 ---REGYAPGTEPHRCKEMSEYESTLCQQLYL 416

RESULT 14
ICE2_MOUSE STANDARD; PRT; 435 AA.
AC P29594; 008737;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-2 precursor (EC 3.4.22.-) (CASP-2) (ICH-1 protease) (NEDD2
protein).
GN CASP2 OR ICH1 OR NEDD2 OR NEDD-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RX MEDLINE=95047319; PubMed=7958843;
RA Kumar S., Kinoshita M., Noda M., Copeland N.G., Jenkins N.A.;
RT "Induction of apoptosis by the mouse Nedd2 gene, which encodes a
RT protein similar to the product of the Caenorhabditis elegans cell
RT death gene ced-3 and the mammalian IL-1 beta-converting enzyme.";
RL Genes Dev. 8:1613-1626(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaebroeck P., Declercq W., van den Brande I.,
RA van Ioo G., Moilemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92328780; PubMed=1378265;
RA Kumar S., Tomooka Y., Noda M.;
RT "Identification of a set of genes with developmentally down-regulated
RT expression in the mouse brain.";
RL Biochem. Biophys. Res. Commun. 185:1155-1161(1992).
CC -1- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Might function by either
CC activating some proteins required for cell death or inactivating
CC proteins necessary for cell survival. May be important in
CC multistep carcinogenesis.
CC -1- SUBUNIT: Heterodimer of a small and a large subunit (by
CC similarity).
CC -1- TISSUE SPECIFICITY: High level expression seen in the embryonic
CC CNS, liver, lung, kidney, small intestine, and hair follicles of
CC vibrissae. Moderate expression seen in the skin, oral mucosa,
CC skeletal muscle, submandibular gland and thymus. In the adult, it
CC is highly expressed in spleen, lung and kidney. Moderately in the
CC brain, heart, testis, liver. Low levels in the thymus, skeletal
CC muscle, ovary and gut.
CC -1- DEVELOPMENTAL STAGE: During embryonic development is highly
CC expressed in several types of mouse tissue undergoing high rates
CC of programmed cell death such as central nervous system and
CC kidney.
CC -1- PTM: THE NATURE PROTEASE CAN PROCESS ITS OWN PROPEPTIDE, BUT NOT
CC THAT OF OTHER CASPASES (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family C14.
CC -1- SIMILARITY: Contains 1 CARD domain.
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CC -----
DR EMBL, D28492; BA02876.1; ALT_INIT.
DR EMBL, Y13085; CA073527.1; ALT_INIT.
DR HSSP; P42574; 1CP3.
DR MEROPS; C14.006; -.
DR MGD; MGI:97295; Casp2.
DR InterPro; IPR001315; CARD.
DR InterPro; IPR002138; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00619; CARD; 1.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; IL1BENZYM.
DR SMART; SM00114; CARD; 1.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50209; CARD; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR HydroLase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 152
FT CHAIN 153 435
FT CHAIN 317 435
FT CHAIN 331 435
FT DOMAIN 15 103
FT ACT_SITE 260 260
FT ACT_SITE 303 303
FT ACT_SITE 303 303
FT CONFLICT 71 71
SQ SEQUENCE 435 AA; 4896 MW; 8984B6AA76E7A676 CRC64;

Query Match 20.8%; Score 101.5; DB 1; Length 435;
Best Local Similarity 31.5%; Pred. No. 0.0033;
Matches 29; Conservative 21; Mismatches 29; Indels 13; Gaps 3;

QY 13 IPTYDALHVSVEGYIAVRHDKGSCFTQTVDFYTK--RKGHILELTYTRMAEA 70
DB 341 LPTPSDMICGACLKGMNAAMRNTRGSGWYIEALTTFVAEDSRDTHVADMVKNVRLKQ- 399
QY 71 ELVDEGKARKTN-----PEIOSTLRRLYL 95
DB 400 ---REGYAPGTEPHRCKEMSEYESTLCQQLYL 428

RESULT 15
ICE6_MOUSE STANDARD; PRT; 276 AA.
AC 008738;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
GN CASP6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/An;
RX MEDLINE=97190206; PubMed=9038361;
RA van de Craen M., Vandenaebroeck P., Declercq W., van den Brande I.,
RA van Ioo G., Moilemans F., Schotte P., van Crielinge W., Beyaert R.,
RA Fiers W.;
RT "Characterization of seven murine caspase family members.";
RL FEBS Lett. 403:61-69(1997).

```

```
CC -!- FUNCTION: Involved in the activation cascade of caspases
CC responsible for apoptosis execution. Cleaves poly(ADP-ribose)
CC polymerase in vitro, as well as lamins. Overexpression promotes
CC programmed cell death (By similarity).
CC -!- SUBUNIT: Heterodimer of a 18 kDa (p18) and a 11 kDa (p11) subunit
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Highly expressed in lung, liver, kidney,
CC testis, and heart. Lower levels in spleen, skeletal muscle and
CC brain.
CC -!- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family C14.
CC -----
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CC -----
DR EMBL: Y13087; CAI73529.1; -.
DR HSSP: P42574; IPAU.
DR MEROPS: C14.005; -.
DR MGD; MGI:1312921; Casp6.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILBCENZIME.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
KW Hydrolase; Thiol protease; Apoptosis; Zymogen.
FT PROPEP 1 5
FT CHAIN 6 162 CASPASE-6 SUBUNIT P18 (BY SIMILARITY).
FT PROPEP 163 176 BY SIMILARITY.
FT CHAIN 177 276 CASPASE-6 SUBUNIT P11 (BY SIMILARITY).
FT ACT_SITE 104 104 BY SIMILARITY.
FT ACT_SITE 146 146 BY SIMILARITY.
SQ SEQUENCE 276 AA; 31595 MW; 5965DE9321126B6C CRC64;
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Query Match 20.7%; Score 101; DB 1; Length 276;
Best local Similarity 32.0%; Pred. No. 0.0022;
Matches 32; Conservative 16; Mismatches 44; Indels 8; Gaps 3;

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QY 2 IVMYIKDSPQITPTTYTDALHVSIVGEGYIAYRHDQKSCFIQTLVDVFTKRKHIL--E 58
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 171 VTGVDAASVYTLTPAGADFLMCGYSVABGYSHRETVNGSWYIQDCEMLA-RYGSLEFTE 229
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 59 LITEVTRMAAEI---VOGKARKTNPEIQSTLRKRLY 94
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 230 LLTLVNRKVSQRVRVDFCKDPDAIGKQVPCFASMLTKKH 269
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
```

Search completed: July 12, 2004, 13:48:23
Job time : 5.76033 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 13:43:31; Search time 19.6364 Seconds

(without alignment)
1542.533 Million cell updates/sec

Title: US-10-068-564-5_COPY_147_242

Sequence: 1 EIVWIKDSQRTPTPTDAL.....KARKNPETLTKRLVIQ 96

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	141.5	29.1	283 13	093417
2	132	27.1	282 13	098018
3	128	26.3	316 5	0817B0
4	128	26.3	426 5	0816Y2
5	127.5	26.2	470 5	09W5E3
6	127.5	26.2	488 5	09UB42
7	127.5	26.2	510 5	081RY7
8	126.5	26.0	488 5	076798
9	126.5	26.0	494 5	076797
10	125	25.7	277 6	08MTC3
11	123	25.3	189 11	08BNT4
12	123	25.3	313 11	08CHV5
13	122	25.1	277 6	08MKT5
14	121	24.8	277 6	095ND5
15	119.5	24.5	476 13	0918J3
16	117	24.0	277 6	08MJU1

17	115	23.6	268 5	Q9TZP6	Q9TZP6 caenorhabdi
18	115	23.6	536 5	018203	018203 caenorhabdi
19	114.5	23.5	289 5	Q86FL0	Q86FL0 anopheles s
20	114.5	23.5	417 5	Q9YIU6	Q9YIU6 pristionchu
21	114	23.4	303 11	088550	088550 rattus norv
22	113	23.2	522 4	Q8IUP5	Q8IUP5 homo sapien
23	112.5	23.1	423 13	Q91B67	Q91B67 xenopus lae
24	111.5	22.9	280 13	Q8UGM9	Q8UGM9 fuigu rubrip
25	111.5	22.9	280 13	Q8JG42	Q8JG42 fuigu rubrip
26	111	22.8	290 13	Q81S68	Q81S68 oryzias lat
27	109.5	22.5	318 13	Q91B65	Q91B65 xenopus lae
28	109	22.4	280 13	Q81T99	Q81T99 oryzias lat
29	107	22.0	328 5	Q81TP3	Q81TP3 branchiosto
30	107	22.0	383 13	Q919L7	Q919L7 brachydantio
31	106.5	21.9	326 5	Q9GV88	Q9GV88 hydra atten
32	103	21.1	276 11	Q9D089	Q9D089 mus musculu
33	102.5	21.0	520 13	Q91B62	Q91B62 xenopus lae
34	102	20.9	303 13	Q91B66	Q91B66 xenopus lae
35	102	20.9	304 13	Q93415	Q93415 gallus gall
36	101.5	20.8	263 5	Q9TZP5	Q9TZP5 caenorhabdi
37	101.5	20.8	452 11	Q8K241	Q8K241 mus musculu
38	101.5	20.8	452 11	Q8C9H7	Q8C9H7 mus musculu
39	101.5	20.8	452 11	Q8C9H7	Q8C9H7 mus musculu
40	101.5	20.8	826 5	Q9Y055	Q9Y055 caenorhabdi
41	101	20.7	276 11	Q99M47	Q99M47 mus musculu
42	101	20.7	454 11	Q9JHK1	Q9JHK1 rattus norv
43	100	20.5	277 11	Q93397	Q93397 rattus norv
44	100	20.5	293 5	Q819V7	Q819V7 bombyx mori
45	100	20.5	454 11	Q9R0T0	Q9R0T0 mus musculu

ALIGNMENTS

RESULT 1
093417 PRELIMINARY; PRT; 283 AA.
ID 093417
AC 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase-3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20149872; PubMed=10684799;
RA Johnson A.L., Bridgman J.T.;
RT "Caspase-3 and -6 expression and enzyme activity in hen granulosa
RT cells".
RT Biol. Reprod. 62:589-598(2000).
DR EMBL; AF083029; AAC32602.1; -.
DR HSSP; P42574; 1PAU.
DR MEROPS; C14.003; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002338; ICE_P10.
DR InterPro; IPR001309; ICE_P20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILBCEZYME.
DR SMART; SM0015; CASc; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS0207; CASPASE_P10; 1.
DR PROSITE; PS0208; CASPASE_P20; 1.
SQ SEQUENCE 283 AA; 31675 MW; 161242DDEFD4DC4F CRC64;
Query Match 29.1%; Score 141.5; DB 13; Length 283;
Best Local Similarity 40.4%; Pred. No. 2.6e-07;

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Matches 36; Conservative 15; Mismatches 33; Indels 5; Gaps 2;
QY 11 QTIPTVTDALHVSIVTVEGYIAYRHDKGSCFIQTLVDVFTK--RKGHILELLETVTRMA 68
Db 192 QKIPVADPEADFLVAYSTAPGYGYSWMNAEGSWFIQSLCRMKEHARKLEMLQILTRVRRVA 251
QY 69 EAEVY---OEGVARKTNPEIQTSLRRRLY 94
Db 252 EYESGSTROPFNKKQIPICTIVSMLTKEFY 280

RESULT 2
Q98UT8
ID Q98UT8 PRELIMINARY; PRT; 282 AA.
AC Q98UT8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
GN CASP3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Yabu T., Okazaki T., Yamashita M.;
RT "Molecular Cloning and Gene Expression of Zebrafish Caspase Related to
RT Mammalian Caspase-3."
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB047003; BAB32409.1; -.
DR HSSP: PA2574; IPAT.
DR MEROPS: C14.003; -.
DR ZFIN: ZDB-GENE-011210-1; casp3.
DR GO: GO:0030693; F:caspase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILIBCNZYME.
DR SMART: SM00115; CASG; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 282 AA; 31522 MW; 13C3454F5E09932E CRC64;

Query Match 27.1%; Score 132; DB 13; Length 282;
Best Local Similarity 36.8%; Pred. No. 2.8e-06;
Matches 35; Conservative 18; Mismatches 36; Indels 6; Gaps 3;
QY 6 IKDPTPTVTDALHVSIVTVEGYIAYRHDKGSCFIQTLVDVFTK--RKGHILELLETV 63
Db 185 IIPGRRIPIEADFLVAYSTVPGYGMKRMNTMSWFIQSLCEMWTXGSLLELQIMTRY 244
QY 64 TRRMA---EAEVQEG-KARKTNPEIQTSLRRRLY 94
Db 245 NKKVALDFESTSNMPPGDAKKQIPICTIVSMLTKEFY 279

RESULT 3
Q817B0
ID Q817B0 PRELIMINARY; PRT; 316 AA.
AC Q817B0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase 3.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
```

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OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RA Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ417903; CAD10676.1; -.
DR GO: GO:0030693; F:caspase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILIBCNZYME.
DR SMART: SM00115; CASG; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 316 AA; 35319 MW; 33A46BCCE6C3F9B7 CRC64;

Query Match 26.3%; Score 128; DB 5; Length 316;
Best Local Similarity 32.3%; Pred. No. 8.9e-06;
Matches 30; Conservative 23; Mismatches 30; Indels 10; Gaps 3;
QY 9 SPQTIPTVTDALHVSIVTVEGYIAYRHDKGSCFIQTLVDVFTK--TKRKHILELLETVTR 66
Db 218 SRALPTPADFLVAYSTVPGYGMKRMNTMSWFIQSLCEMWTXGSLLELQIMTRY 277
QY 67 MAEAEVQEGKARKTNPEIQ---STURKRLYLQ 96
Db 278 VA-----YDFQGRGRKKQIIPAVYMLTRKLYFR 305

RESULT 4
Q816Y2
ID Q816Y2 PRELIMINARY; PRT; 426 AA.
AC Q816Y2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Caspase-3.
GN CASP-3L.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Eukaryota;
RC Wiens M., Saenger H., Krasko A., Perovic S., Mueller W.E.G.;
RT "Caspase-mediated apoptosis in sponges: cloning and function.";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ344144; CAC83013.1; -.
DR GO: GO:0030693; F:caspase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR002138; ICE_p10.
DR InterPro: IPR001309; ICE_p20.
DR InterPro: IPR002398; Peptidase_C14.
DR Pfam: PF00656; Peptidase_C14; 1.
DR PRINTS: PR00376; ILIBCNZYME.
DR SMART: SM00115; CASG; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
SQ SEQUENCE 426 AA; 48024 MW; 713B5EEC82BED0C1 CRC64;

Query Match 26.3%; Score 128; DB 5; Length 426;
Best Local Similarity 32.3%; Pred. No. 1.3e-05;
Matches 30; Conservative 23; Mismatches 30; Indels 10; Gaps 3;
QY 9 SPQTIPTVTDALHVSIVTVEGYIAYRHDKGSCFIQTLVDVFTK--TKRKHILELLETVTR 66
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DB      328 SRRLPTLADFLVLAIVTPEYVSWRNSEVGFIXFVDMRLASKEHMDILTEVNRK 387
QY      67 MAEALVQSGKARKNTPEIO---STRKRLYLQ 96
DB      388 VA-----YDFQSRGRNKOIPAPVTMLTRKLYFR 415

RESULT 5
Q9WSE3  PRELIMINARY; PRT; 470 AA.
AC Q9WSE3; 002433;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Caspase-8/-10 Homolog (DREDD).
GN DREDD OR DCP2D OR EG:115C2.9 OR CG7486.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=RAS V RPI1215(C4);
RX MEDLINE=98021435; PubMed=9380701;
RA Inohara N., Koseki T., Hu Y., Chen S., Nunez G.;
RT "CLARP, a death effector domain-containing protein interacts with
RT caspase-8 and regulates apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:10717-10722(1997).
[2]

RN (2)
RP SEQUENCE OF 104-470 FROM N.A.
RA Chen P., Rodriguez A., Erskine R., Thach T., Abrams J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031652; AAC15843.1; -.
DR EMBL; AF070716; AAC31214.1; -.
DR HSSP; Q15806; 10DU.
DR FlyBase; FBgn020381; Dredd.
DR GO; GO:0004200; P:signaling (initiator) caspase activity; NAS.
DR GO; GO:0006632; P:apoptotic program; IEP.
DR GO; GO:0006952; P:defense response; IMP.
DR InterPro; IPR00138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; I.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 470 AA; 53412 MW; F9CDB4F1B1CED9ED CRC64;

Query Match 26.2%; Score 127.5; DB 5; Length 470;
Best Local Similarity 37.2%; Pred. No. 1.6e-05;
Matches 32; Conservative 12; Mismatches 27; Indels 15; Gaps 3;

QY      16 YTDALHYSTVEGYIAYRHDDGSCFIQTIVDVFTKRG--HLELLTEVTRMAEALV 73
DB      388 HIDMLRAMSTVNGVYALHHTQTGWSFISLCDAIRRSASEHIDILITVNEVS----- 442
QY      74 QEGKARKTN-----PEIOSTRKRLYL 94
DB      443 ---KKRGSNDSEWVNVKSTRQHY 465

RESULT 6
Q9UB42  PRELIMINARY; PRT; 488 AA.
AC Q9UB42;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE EG:115C2.9 protein.
GN DREDD OR EG:115C2.9 OR CG7486.

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OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN (1)
RP SEQUENCE FROM N.A.
RA Catherine Salles, Philippe Valenti, Areti Darlamtsou,
RA Nadine Henderson, Jorna Campbell, David Glover;
RT "Sequencing the distal X chromosome of Drosophila melanogaster.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
[2]

RN (2)
RP SEQUENCE FROM N.A.
RA Benos P.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031581; CAA20893.1; -.
DR PIR; T13385; T13385.
DR HSSP; Q15806; 10DU.
DR FlyBase; FBgn020381; Dredd.
DR GO; GO:0004200; P:signaling (initiator) caspase activity; NAS.
DR GO; GO:0006632; P:apoptotic program; IEP.
DR GO; GO:0006952; P:defense response; IMP.
DR InterPro; IPR002398; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; I.
DR PRINTS; PR00376; ILIBENZYM.
DR SMART; SM00115; CASc; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 488 AA; 55450 MW; 5D444C8D2DFA06 CRC64;

Query Match 26.2%; Score 127.5; DB 5; Length 488;
Best Local Similarity 37.2%; Pred. No. 1.7e-05;
Matches 32; Conservative 12; Mismatches 27; Indels 15; Gaps 3;

QY      16 YTDALHYSTVEGYIAYRHDDGSCFIQTIVDVFTKRG--HLELLTEVTRMAEALV 73
DB      406 HIDMLRAMSTVNGVYALHHTQTGWSFISLCDAIRRSASEHIDILITVNEVS----- 460
QY      74 QEGKARKTN-----PEIOSTRKRLYL 94
DB      461 ---KKRGSNDSEWVNVKSTRQHY 483

RESULT 7
Q8IRY7  PRELIMINARY; PRT; 510 AA.
AC Q8IRY7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CG7486-PA.
GN DREDD OR EG:115C2.9 OR CG7486.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RN (1)
RP SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
RA Abail J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
RA Baillet R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhargava D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

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RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris N., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Houtin D., Houston K.A., Howland T.J., Wei M.H., Ibeagwa C., Jallali M., Kalush P., Kapen G.L., Ke Z., Kemson J.A., Kechum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Matea B., McIntosh T.C., McLeod M.P., McPherson D., Meekulov G., Mishina N.V., Mobarry C., Morris D., Moshirei A., Mount S.M., Moy M., Murphy B., Murphy L., Murzy D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R., Scheeler F., Shen H., Shne B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G.C., Wu D., Yang S., Yao Q.A., Ye J., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,"	RA	"The genome sequence of Drosophila melanogaster.";	RL	Science 287:2185-2195(2000).	RP	SEQUENCE FROM N.A.	RA	Celniker S.E., Adams M.D., Krommler B., Wan K.H., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Bazzon J., An H., Baldwin D., Banazon J., Beeson K.T., Buesam D.A., Carlson J.W., Catter A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsetti V., Doup L.E., Doyle C., Drenek D., Farfan D., Ferreira S., Frise E., Galle R.F., Gay N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibeagwa C., Jallali M., Kense D., Li P., Matea B., Moshirei A., McIntosh T.C., Moy M., Murphy B., Nelson K.A., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanavong S., Piltman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,"	RL	"Sequencing of Drosophila melanogaster genome.";	RP	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	RA	SEQUENCE FROM N.A.	RA	Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochack S.E., Smith C.D., Tupy J.L., Bergman C., Bertan B., Carlson J.W., Celniker S.E., Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Krommler B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.U., Lewis S.E.,"	RL	"Annotation of Drosophila melanogaster genome.";	RP	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	RA	SEQUENCE FROM N.A.	RA	Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.,"	RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	RP	SEQUENCE FROM N.A.	RA	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.	RL	EMBL: AE003418; AAN09022.1; "	RP	FLYBase; FBgn0020381; Dredd.	DR	GO; GO:0004200; F:signaling (initiator) caspase activity; NAS.	DR	GO; GO:0008632; P:apoptotic program; IEP.	DR	GO; GO:0006952; P:defense response; IMP.	DR	InterPro: IPR002138; ICG p10.	DR	InterPro: IPR002398; Peptidase C14.	DR	Pfam: PF00656; Peptidase C14; I.	DR	PRINTS; PR00376; ILIBENZYME.											
DR	SMART; SM00115; CASc; 1.	DR	PROSITE; PS50207; CASPASE_P10; 1.	DR	PROSITE; PS50208; CASPASE_P20; 1.	DR	SEQUENCE 510 AA; 57956 MW; 1CEBBD5728DC8BA2 CRC64;	QY	Query Match	26.2%;	Score 127.5;	DB 5;	Length 510;	Best Local Similarity	37.2%;	Pred. No. 1.8e-05;	Matches	32;	Conservative	12;	Mismatches	27;	Indels	15;	Gaps	3;	Db	428	HIDMLRAMSTVNGYAAIRHTQTSWFTGSLCDAIRRSASHEIADILITVNEVS-----	482	QY	16	YTDALHVSIVTVEGYIAYRHDKGSCFIOTLVDFVTFKRGK--HILELITVEVTRMAAEVL	73	Db	428	HIDMLRAMSTVNGYAAIRHTQTSWFTGSLCDAIRRSASHEIADILITVNEVS-----	482	QY	74	QEGKARKTN-----PEIOSTLTKRLY	94	Db	461	---KKRGSNDESWVNPVNSTFRQHYV	483	RESULT 9	076797	PRELIMINARY;	PRT;	494	AA.	AC	076797;	AC	01-NOV-1998 (TReMBLrel. 08, Created)	DT	01-NOV-1998 (TReMBLrel. 08, Last sequence update)	DT	01-NOV-1998 (TReMBLrel. 08, Last sequence update)

	Query Match	26.0%	Score 126.5	DB 5	Length 494
	Best Local Similarity	37.2%	Pred. No. 2,2e+05		
	Matches	Conservative 32	Mismatches 11	Gaps 28	Indels 15
Oy	16	YTDALHYSTEGVGYAARHDKDQSGEIQITVDVFYFKRG--HILELLEIVRRRAAEELV	73		
		: : : : : : : : : : : : : : : : : :			
Dd	412	HIDILRAMSTNGYAAALRHRTQTGSFISLCDAIDRKASSEHIADILITVNEVS----	466		
Oy	74	OEGRARKTN-----PEIOSLRKRLRY	94		
		: : : : : : : : : : : : : : : : : :			
Dd	467	---KKRGSNDSEWPNVNSTRFOHY	489		

RESULT 10			
08MJC3			
ID	08MJC3	PRELIMINARY;	EFT; 277 AA.
AC	08MJC3;		
DT	01-OCT-2002	(TREMBLrel. 22, Created)	
DT	01-OCT-2002	(TREMBLrel. 22, last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, last annotation update)	
DE	Cysteine protease CPP32.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=98236830; PubMed=9575916;		
RA	Wang H., Keiser J.A.;		
RT	"Molecular characterization of rabbit CPP32 and its function in		
RL	vascular smooth muscle cell apoptosis.";		
RL	Am. J. Physiol. 274:H1132-H1140(1998).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RA	Wang H., Keiser J.A.;		
RT	Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.		
RA	EMBL; AF506008; AAM47195.1; -;		
DR	GO; GO:0030693; F:caspase activity; IEA.		
DR	GO; GO:0008233; F:peptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR002138; ICE_P10.		
DR	InterPro; IPR001309; ICE_P20.		
DR	InterPro; IPR002398; Peptidase C14.		

QY 11 QITPTYDADAHVSTVGATYAIRDQSCSIQTLVAVFTTRKHILE---LITEVPRM 67
 Db 185 QKIVPADFLVASTAGYTSWNRSEGSWFIQLC-AMLEKVAHKEFPHILIRVRNVK 243
 QY 68 A----EALVQEGARKTNPICSTLKKRLY 94
 Db 244 ATEFESYSTLATTHAKQIPOLVSMLEKELY 274

[illegible]

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RESULT 12
Q8CHV5 PRELIMINARY; PRT; 313 AA.
AC Q8CHV5;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase 3, apoptosis related cysteine protease (fragment).
GN CASP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Strausberg R.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
EMBL; BC038825; AA038825.1; -.
DR MGD; MGI:107739; Casp3.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
DR PROTEASE.
KW NON TER.
FT
SQ SEQUENCE 313 AA; 35174 MW; 96B98A1F04E769FC CRC64;

Query Match 25.3%; Score 123; DB 11; Length 313;
Best Local Similarity 39.6%; Pred. No. 3.1e-05;
Matches 36; Conservative 11; Mismatches 36; Indels 8; Gaps 3;

QY 11 QITPTTDLAHVSTVEGTAYARHDQSGCFIQTVDVFTKRKGHILE--LTETVRM 67
DB 221 QKLPVADFLYASTAPGYTSWRNSKDSWFIQSLCAAL-KQYVHKLEIHWIILRVNRKV 279
QY 68 A---EAEIVQEGKARKTNEIQTSLRKRLY 94
DB 280 ATEFESFSDSTFHAKKQIPCIYSMLTKELY 310

RESULT 13
Q8MK15 PRELIMINARY; PRT; 277 AA.
AC Q8MK15;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase-3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC Sano J.;
RA "canine caspase-3 gene";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AB085580; BAB92962.1; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.

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DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31334 MW; 7094C76D868BDBA9 CRC64;

Query Match 25.1%; Score 122; DB 6; Length 277;
Best Local Similarity 41.3%; Pred. No. 3.5e-05;
Matches 38; Conservative 10; Mismatches 36; Indels 8; Gaps 4;

QY 11 QITPTTDLAHVSTVEGTAYARHDQSGCFIQTVDVFTKRKGHILE--LTETVRM 67
DB 185 QKLPVADFLYASTAPGYTSWRNSKDSWFIQSLCAAL-KQYVHKLEIHWIILRVNRKV 243
QY 68 A-EAEIVQEGKA---RKTNPEIQSTLRKRLYL 95
DB 244 ATEFESFSDSAFHGKKQIPCIYSMLTKELY 275

RESULT 14
Q95ND5 PRELIMINARY; PRT; 277 AA.
AC Q95ND5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Caspase-3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=21334413; PubMed=1140638;
RA Muneta Y., Shimojima Y., Mori Y.;
RT "Porcine caspase-3: cloning and its activity during apoptosis of
  porcine PK15 cells induced by porcine Fas-ligand.";
RL J. Interferon Cytokine Res. 21:409-415 (2001).
DR EMBL; AB029345; BAB5544.1; -.
DR MEROPS; C14.003; -.
DR GO; GO:0030693; F:caspase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002138; ICE_p10.
DR InterPro; IPR001309; ICE_p20.
DR InterPro; IPR002398; Peptidase_C14.
DR Pfam; PF00656; Peptidase_C14; 1.
DR PRINTS; PR00376; ILIBCEZYME.
DR SMART; SM00115; CASG; 1.
DR PROSITE; PS01122; CASPASE_CYS; 1.
DR PROSITE; PS01121; CASPASE_HIS; 1.
DR PROSITE; PS50207; CASPASE_P10; 1.
DR PROSITE; PS50208; CASPASE_P20; 1.
SQ SEQUENCE 277 AA; 31379 MW; 616C0F56141B012B CRC64;

Query Match 24.8%; Score 121; DB 6; Length 277;
Best Local Similarity 41.8%; Pred. No. 4.5e-05;
Matches 38; Conservative 10; Mismatches 35; Indels 8; Gaps 4;

QY 11 QITPTTDLAHVSTVEGTAYARHDQSGCFIQTVDVFTKRKGHILE--LTETVRM 67
DB 185 QKLPVADFLYASTAPGYTSWRNSKDSWFIQSLCAAL-KQYVHKLEIHWIILRVNRKV 243
QY 68 A-EAEIVQEGK---ARKTNEIQTSLRKRLY 94
DB 244 ATEFESFSDSTFHAKKQIPCIYSMLTKELY 274

RESULT 15

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ID	Q91873	PRELIMINARY;	PRT;	476 AA.
AC	Q91873;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)			
DE	Caspase-8.			
GN	CASP8.			
OS	Brachydanio rerio (Zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxID=7955;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20373792; PubMed=10917738;			
RA	Inohara N., Nunez G.;			
RT	"Genes with homology to mammalian apoptosis regulators identified in zebrafish."			
RL	Cell Death Differ. 7:509-510 (2000) .			
DR	EMBL; AF273220; AAF79207.1; --			
DR	HSSP; Q15806; 10DT.			
DR	MEROPS; C14.009; --			
DR	ZFIN; ZDR-GENE-0007713-1; casp8.			
DR	GO; GO:0016329; F:apoptosis regulator activity; IEA.			
DR	GO; GO:0030693; F:caspase activity; IEA.			
DR	GO; GO:0006915; F:apoptosis; IEA.			
DR	GO; GO:0006508; F:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR001875; DED.			
DR	InterPro; IPR002138; ICE p10.			
DR	InterPro; IPR001309; ICE p20.			
DR	InterPro; IPR002398; Peptidase_C14.			
DR	Pfam; PF01335; DED; 2.			
DR	Pfam; PF00656; Peptidase_C14; 1.			
DR	PRINTS; PR00376; IL1BCEZYME.			
DR	SMART; SM00115; CASC; 1.			
DR	SMART; SM00031; DED; 2.			
DR	PROSITE; PS01122; CASPASE_CYS; 1.			
DR	PROSITE; PS0207; CASPASE_P10; 1.			
DR	PROSITE; PS0208; CASPASE_P20; 1.			
DR	PROSITE; PS0168; DED; 2.			
SQ	SEQUENCE 476 AA; 54890 MW; FQ9DFFA4B3GC1IFB9 CRC64;			

